

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:23:52 ; Search time 11 Seconds
(without alignments)
192.209 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKDLGKRLMESHGFE.....MIVECMNATCTRVYKQV 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	713	100.0	135 10	US-09-788-074-1
2	612	85.8	135 10	US-09-788-074-3
3	380	53.3	132 10	US-09-901-436A-11
4	362	50.8	132 10	US-09-905-235-1
5	333	46.7	132 10	US-09-986-240-2
6	333	46.7	133 10	US-09-901-436A-10
7	333	46.7	133 12	US-10-153-740-13
8	320	44.9	133 12	US-10-153-740-12
9	318	44.6	133 10	US-09-901-436A-7
10	318	44.6	133 12	US-10-153-740-11
11	292	41.0	132 10	US-09-971-187-2
12	280.5	39.3	131 12	US-10-153-740-15
13	219.5	30.8	149 10	US-09-925-302-496
14	214.5	30.1	138 9	US-09-736-457-328
15	193	27.1	160 10	US-09-925-301-848
16	186	26.1	135 10	US-09-901-436A-8
17	184	25.8	135 10	US-09-737-149-48
18	184	25.8	135 12	US-10-153-740-2
19	182	25.5	135 10	US-09-737-149-49

20	181	25.4	135	10	US-09-737-149-16	Sequence 16, Appl
21	150	21.0	134	10	US-09-901-436A-9	Sequence 9, Appl
22	138	19.4	156	10	US-09-737-149-14	Sequence 14, Appl
23	133	18.7	107	10	US-09-901-436A-2	Sequence 2, Appl
24	123.5	17.3	106	12	US-10-153-740-14	Sequence 14, Appl
25	114	16.0	70	10	US-09-737-149-46	Sequence 46, Appl
26	114	16.0	70	10	US-09-737-149-47	Sequence 47, Appl
27	91.5	12.8	997	10	US-09-747-371-3	Sequence 3, Appl
28	83	11.6	614	10	US-09-782-051-2	Sequence 2, Appl
29	76	10.7	26	10	US-09-347-064-14	Sequence 14, Appl
30	73.5	10.3	999	10	US-09-747-371-2	Sequence 2, Appl
31	72	10.1	396	10	US-09-837-751-2	Sequence 2, Appl
32	71	10.0	127	9	US-09-981-353-21	Sequence 21, Appl
33	71	10.0	253	10	US-09-815-242-10279	Sequence 10279, A
34	70	9.8	1426	10	US-09-912-020-340	Sequence 340, App
35	69	9.7	253	10	US-09-815-242-13878	Sequence 13878, A
36	67	9.4	1499	10	US-09-911-826A-2	Sequence 2, Appl
37	66.5	9.3	429	10	US-09-742-954-12	Sequence 12, Appl
38	66.5	9.3	758	10	US-09-903-248-2	Sequence 2, Appl
39	66.5	9.3	758	10	US-09-859-604-2	Sequence 2, Appl
40	66.5	9.3	758	10	US-09-903-063-2	Sequence 2, Appl
41	66.5	9.3	758	10	US-09-903-216-2	Sequence 2, Appl
42	66.5	9.3	758	10	US-09-903-199-2	Sequence 2, Appl
43	66.5	9.3	758	10	US-09-903-023-2	Sequence 2, Appl
44	65.5	9.2	750	10	US-09-402-100-2	Sequence 2, Appl
45	65.5	9.2	832	10	US-09-919-585-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-788-074-1
; Sequence 1, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:
; APPLICANT: Holamislil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MALL
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-074-1

Query Match	100.0%	Score 713:	DB 10:	Length 135:
Best Local Similarity	100.0%	Pred No. 2.7e-71:		
Matches 135:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Qy	1	MASLKDLGKRLMESHGFEYMKELGVLARKMAAKPDCIITCDGNNITVKTESTV	60	
Db	1	MASLKDLGKRLMESHGFEYMKELGVLARKMAAKPDCIITCDGNNITVKTESTV	60	
Qy	61	KTVFSCNLGKFPDETADGRKTCTTODGALVOHQWDGKRESTITRKLKDGKMIVEC	120	
Db	61	KTVFSCNLGKFPDETADGRKTCTTODGALVOHQWDGKRESTITRKLKDGKMIVEC	120	
Qy	121	VMNATCTRVYKQV	135	
Db	121	VMNATCTRVYKQV	135	
RESULT 2				
US-09-788-074-3				
; Sequence 3, Application US/09788074				
; Patent No. US20010044110A1				
; GENERAL INFORMATION:				


```
Db      127 RTYEK 131          |||

RESULT 10
US-10-153-740-11
; Sequence 11, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
;              YU, GUO-LIANG
;              GEINTEZ, REINER L.
;              DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
US-10-153-740-11
Query Match           44.6%; Score 318; DB 12; Length 133;
Best Local Similarity 47.2%; Pred. No. 5.7e-28;
Matches 59; Conservative 27; Mismatches 39; Indels 0; Gaps 0

Qy    9 GKWLMPESHGFEYMKELGVGLALRKMAAMAKPDCIIITCDGNNTIVKTSTVKTTFVSCN 68
      |:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    7 GTWKLVDKSNFDYYMKSGLVGFGFATROVASMTKPTTIEKNGDFTITIKTQSTFKNTINFQ 66
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy    69 LGKKFDETTADGRKTEVTVCFFQDGLAVHOHQWDGKESTTRKLLKDGCKMLVECVMNNACT 128
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    67 LGLEFDEVETADDRKRVKSLVTLDDGGKLIHVQKWNGQETTTLRELVDGKILTLTHGSVVST 126
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy    129 RVYEK 133
      |::|||
Db    127 RTYEK 131

RESULT 11
US-09-971-187-2
Sequence 2, Application US/09971187
```



```
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-328

Query Match      30.1%; Score 214.5; DB 9; Length 138;
Best Local Similarity 34.8%; Pred. No. 1.4e-16;
Matches 47; Conservative 36; Mismatches 45; Indels 7; Gaps 4;

QY  4  LKDLGKWLMEHSGFEYMKELGVGLALRK--MAAMAKPDCIITCDGNNITVKTSTVK 61
DB  1  MFNFGNKKIIRSENFPELLKVLGVNMLRKIAVAASAKPAVEIKOEGDTFYIKTSTVR 60

QY  62  TTVFSCNLGKPFDETTADGRKTETVCTFQ-DGALVHQH---QWDGKSEITIRKL-KDGKM 116
DB  61  TTEINFKVGEEFEQTVDCRCKSLVKWSESNKMVCEQKLLKGEKPKTSWRELNDGEL 120

QY  117  IVECVNNAATCTRVY 131
DB  121  ILTMTADDVVCTRY 135

RESULT 15
US-09-925-301-848
; Sequence 848, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925.301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 848
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-848

Query Match      27.1%; Score 193; DB 10; Length 160;
Best Local Similarity 36.1%; Pred. No. 3.8e-14;
Matches 44; Conservative 27; Mismatches 45; Indels 6; Gaps 2;

QY  16  SHGFEEYMKELGVGLALRK--MAAMAKPDCIITCDGNNITVKTSTVKTVFSCNLGKXF 73
DB  36  SENFDELLKALGVNAMLRKVAVAASAKPHVEIRQDQDFYIKTSTVTRTEINFKVGEGF 95
```

```
QY  74  DETTADGRKTETVCTFQDGALVHQH---WDGKSEITIRKLKGKMIVECVNNAATCTR 129
DB  96  BEETVDGRKCRSLATWENENKIHCTQTLLLEGDPKTYWTRELANDELILITFGADDDVCTR 155

QY  130  VY 131
DB  156  IV 157

Search completed: November 25, 2002, 10:25:45
Job time : 12 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:23:07 ; Search time 15 Seconds
(without alignments)
264.806 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKDEGKRLMESHGFE.....MIVECVNNATCTRVYKQV 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	612	85.8	135	1	US-08-446-600A-4
2	380	53.3	132	1	US-08-409-731A-11
3	380	53.3	132	2	US-08-470-298B-11
4	380	53.3	132	2	US-09-023-073A-11
5	380	53.3	132	4	US-09-361-737-11
6	333	46.7	133	1	US-08-409-731A-10
7	333	46.7	133	2	US-08-470-298B-10
8	333	46.7	133	2	US-08-820-825-13
9	333	46.7	133	2	US-09-023-073A-10
10	333	46.7	133	4	US-09-307-817-13
11	333	46.7	133	4	US-09-361-737-10
12	333	46.7	133	4	US-09-734-036-13
13	320	44.9	133	2	US-08-820-825-12
14	320	44.9	133	4	US-09-307-817-12
15	320	44.9	133	4	US-09-734-036-12
16	318	44.6	131	1	US-08-409-731A-7
17	318	44.6	131	2	US-08-470-298B-7
18	318	44.6	133	2	US-08-820-825-11
19	318	44.6	133	2	US-09-023-073A-7
20	318	44.6	133	4	US-09-307-817-11
21	318	44.6	133	4	US-09-361-737-7
22	318	44.6	133	4	US-09-734-036-11
23	292	41.0	132	4	US-09-043-646-2
24	280.5	39.3	131	2	US-08-820-825-15
25	280.5	39.3	131	4	US-09-307-817-15
26	280.5	39.3	131	4	US-09-734-036-15
27	271	38.0	132	2	US-08-470-298B-12

28	214.5	30.1	138	1	US-08-468-709B-2	Sequence 2, Appli
29	214.5	30.1	138	2	US-08-241-664B-2	Sequence 2, Appli
30	214.5	30.1	138	5	PCT-US93-03936-2	Sequence 2, Appli
31	213	29.9	137	1	US-08-468-709B-4	Sequence 4, Appli
32	213	29.9	137	2	US-08-241-664B-4	Sequence 4, Appli
33	213	29.9	137	5	PCT-US93-03936-4	Sequence 4, Appli
34	210.5	29.5	138	1	US-08-468-709B-12	Sequence 12, Appli
35	210.5	29.5	138	2	US-08-241-664B-12	Sequence 12, Appli
36	210	29.5	137	1	US-08-468-709B-11	Sequence 11, Appli
37	210	29.5	137	2	US-08-241-664B-11	Sequence 11, Appli
38	197.5	27.7	133	1	US-08-554-463-1	Sequence 1, Appli
39	187	26.2	135	1	US-08-409-731A-8	Sequence 8, Appli
40	187	26.2	135	2	US-08-470-298B-8	Sequence 8, Appli
41	187	26.2	135	2	US-08-847-724-4	Sequence 4, Appli
42	186	26.1	135	2	US-08-847-724-6	Sequence 6, Appli
43	186	26.1	135	2	US-09-023-073A-8	Sequence 8, Appli
44	186	26.1	135	3	US-08-899-031-4	Sequence 4, Appli
45	186	26.1	135	4	US-09-361-737-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-446-600A-4
; Sequence 4, Application US/08446600A
; Patent No. 5719126
; GENERAL INFORMATION:
; APPLICANT: NO. 5719126dlund, James J. and Farooqui, Jamal Z.
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frost & Jacobs
; STREET: 2500 PNC Center, 201 East Fifth St.
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45202-4182
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,600A
; FILING DATE: 24 May 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,513
; FILING DATE: 24 No. 5719126ember 1992
; APPLICATION NUMBER: PCT/US93/11139
; FILING DATE: 16 No. 5719126ember 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann G. Robinson
; REGISTRATION NUMBER: 39,820
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 651-6128
; TELEFAX: (513) 651-6981
; TELEX: 21-4396 F&J Cln
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; US-08-446-600A-4

Query Match 85.8%; Score 612; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 6.2e-66;
Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
QY 1 MASLKDEGKRLMESHGFEYKELGVLALRKMAAKPDCITTCGDNNTVKTSTV 60

Db 1 MATVQLEGRWLRVDSKGFDEYMKELGVGLALRKMAMAKPDCIITCDGKNLTIKTESTL 60
QY 61 KTVFSCNIGKEFDETTADGRKRTETVCTFDGALVQHQWDGKESIITRKLKDGKMIVEC 120
Db 61 KTVFSCNIGKEFDETTADGRKRTETVCTFDGALVQHQWDGKESIITRKLKDGKMIVEC 120
QY 121 VMNATCTRIYKVK 135
Db 121 VMNATCTRIYKVK 135

RESULT 2

US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PFI75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-409-731A-11

Query Match 53.3%; Score 380; DB 1; Length 132;
Best Local Similarity 56.3%; Pred. No. 4, 4e-38;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEEYMKELGVGLALRKMAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLAKEPTVIISKKGDIITRTSTFKNTEISFK 66
QY 69 LGKEFDETTADGRKRTETVCTFDGALVQHQWDGKESIITRKLKDGKMIVECVMNATCT 128
Db 67 LGQEFETADNRKTKSVITLQRLGSLNQRWDGKETTIRKLKLVNGKMYAECKMKGVVCT 126
QY 129 RYVEKV 134
Db 127 RYVEKV 132

RESULT 3

US-08-470-298B-11
; Sequence 11, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,298B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PFI75D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: MYELIN P2 (FIGURE 2)
US-08-470-298B-11

Query Match 53.3%; Score 380; DB 2; Length 132;
Best Local Similarity 56.3%; Pred. No. 4, 4e-38;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEEYMKELGVGLALRKMAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLAKEPTVIISKKGDIITRTSTFKNTEISFK 66
QY 69 LGKEFDETTADGRKRTETVCTFDGALVQHQWDGKESIITRKLKDGKMIVECVMNATCT 128
Db 67 LGQEFETADNRKTKSVITLQRLGSLNQRWDGKETTIRKLKLVNGKMYAECKMKGVVCT 126
QY 129 RYVEKV 134
Db 127 RYVEKV 132

RESULT 4

US-09-023-073A-11
; Sequence 11, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,073
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-361-737-11

Query Match 53.3% Score 380; DB 4; Length 132;
Best Local Similarity 56.3%; Pred. No. 4.4e-38;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;

QY 9 GKWLMEHSGHFEFYMKELGVGLALRKMAAMAKPCITCDGNITVTKTESVKTTFVSCN 68
DB 7 GTWKLVSSENFDDYMKALGVGLATRKLGNAKPTVIISKKGDIITRTESIFKNTESISFK 66

QY 69 LGKEFDETTADGRTEVTCVTFQDQALVQHQQMDGKESTITRKLDGKMKVIVCVNNATCT 128
DB 67 LGQFEETTDNRKTKSVITLQRLSNQVQRWDGKETITKRKLNGKMAVECKMKGVVCT 126

QY 129 RVYEKV 134
DB 127 RIYEKV 132

RESULT 6
US-08-409-731A-10
; Sequence 10, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,731A
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PF175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:

```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-409-731A-10

Query Match          46.7%; Score 333; DB 1; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;

QY 9 GKWRLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTVKTTFVSCN 68
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPKPTTIIKNGDILTLKTHSTFKNTEISFK 66
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 69 LGKEFDETTADGRKTTVCTFODGALVQHQWGDGKESTITRKLKDGKMIVECVMMNATCT 128
   ||:::||||| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 67 LGVEFDETTADDRKVKSVITLDGGKLVHLQKWGDGQETTLVRELIDGKLILTLTHGTA VCT 126
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 129 RYVEK 133
   |:::|
Db 127 RYVEK 131
   |:::|

RESULT 7
US-08-470-298B-10
; Sequence 10, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: FABP (FIGURE 2)
US-08-470-298B-10

Query Match          46.7%; Score 333; DB 2; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 9 GKWRLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTVKTTFVSCN 68
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPKPTTIIKNGDILTLKTHSTFKNTEISFK 66
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 69 LGKEFDETTADGRKTTVCTFODGALVQHQWGDGKESTITRKLKDGKMIVECVMMNATCT 128
   ||:::||||| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 67 LGVEFDETTADDRKVKSVITLDGGKLVHLQKWGDGQETTLVRELIDGKLILTLTHGTA VCT 126
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 129 RYVEK 133
   |:::|
Db 127 RYVEK 131
   |:::|

RESULT 8
US-08-820-825-13
; Sequence 13, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-13

Query Match          46.7%; Score 333; DB 2; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 9 GKWRLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTVKTTFVSCN 68
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPKPTTIIKNGDILTLKTHSTFKNTEISFK 66
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 69 LGKEFDETTADGRKTTVCTFODGALVQHQWGDGKESTITRKLKDGKMIVECVMMNATCT 128
   ||:::||||| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 67 LGVEFDETTADDRKVKSVITLDGGKLVHLQKWGDGQETTLVRELIDGKLILTLTHGTA VCT 126
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 129 RYVEK 133
   |:::|
Db 127 RYVEK 131
   |:::|
```

```
RESULT 9
US-09-023-073A-10
; Sequence 10, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.073A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PFI75D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-073A-10

Query Match 46.7%; Score 333; DB 2; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;

Qy 9 GKRLMESHGFEYMKELGVGLALRKMAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRQVASMTKPTTIIIEKNGDILTTLKTHSTFKNTEISFK 66

Qy 69 LGKEFDETTADGRKTETVCTFDGALVHQWQDGGKSTITRKLKDGKMIKVECMNATCT 128
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 67 LGVEFDETTADGRKVSIVTLDGGKLVHLQKWQDGETTLVRELIDGKLILTLTHGTAVCT 126

Qy 129 RYVEK 133
| : : : : |
Db 127 RYVEK 131

RESULT 10
US-09-307-817-13
; Sequence 13, Application US/09307817
; Patent No. 6232291
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307.817
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-307-817-13

Query Match 46.7%; Score 333; DB 4; Length 133;
Best Local Similarity 50.4%; Pred. No. 2e-32;
Matches 63; Conservative 23; Mismatches 39; Indels 0; Gaps 0;

Qy 9 GKRLMESHGFEYMKELGVGLALRKMAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRQVASMTKPTTIIIEKNGDILTTLKTHSTFKNTEISFK 66

Qy 69 LGKEFDETTADGRKTETVCTFDGALVHQWQDGGKSTITRKLKDGKMIKVECMNATCT 128
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 67 LGVEFDETTADGRKVSIVTLDGGKLVHLQKWQDGETTLVRELIDGKLILTLTHGTAVCT 126

Qy 129 RYVEK 133
| : : : : |
Db 127 RYVEK 131

RESULT 11
US-09-361-737-10
; Sequence 10, Application US/09361737
; Patent No. 6287812
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307.817
```

7T-C78-078-80-50

Search completed: November 25, 2002, 10:25:28
Job time : 16 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:22:52 ; Search time 17 Seconds
(without alignments)
763.420 Million cell updates/sec

Title: US-09-788-074-1

Perfect score: 713

Sequence: 1 MASLKDEGKWRMLMESHGFE.....MIVECVMNATCTRVYEVQ 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	713	100.0	135	2 A47497	lipid-binding prot
2	663	93.0	135	2 JC2201	fatty acid-binding
3	612	85.8	135	2 I56326	fatty acid binding
4	391	54.8	132	1 MPRB2	myelin P2 protein
5	380	53.3	132	1 MPRU2	myelin P2 protein
6	375	52.6	132	2 S77744	adipocyte-type fat
7	369	51.8	132	2 JH0407	myelin P2 protein
8	367	51.5	131	1 MPBO2	myelin P2 protein
9	364	51.1	132	2 S20297	fatty acid-binding
10	362	50.8	132	1 F2HUF	fatty acid-binding
11	357	50.1	132	2 B25952	myelin P2 protein
12	336	47.1	133	2 A27452	fatty acid-binding
13	333	46.7	133	1 F2HUC	fatty acid-binding
14	320	44.9	132	2 I52524	testis lipid bindi
15	320	44.9	133	2 A34676	fatty acid-binding
16	318	44.6	133	2 PC4011	fatty acid-binding
17	308	43.2	132	2 A49184	fatty acid-binding
18	302	42.4	131	2 S06479	fatty acid-binding
19	282	39.6	132	2 I58161	lipid-binding prot
20	282	39.6	132	2 I48923	fatty acid-binding
21	281	39.4	132	2 I56510	fatty acid binding
22	235.5	33.0	137	2 T25123	hypothetical prote
23	234.5	32.9	136	2 T15207	hypothetical prote
24	233.5	32.7	135	2 T15205	hypothetical prote
25	216.5	30.4	138	2 A42495	retinoic acid-bind
26	216.5	30.4	138	2 I51265	xCRABP - African c
27	214.5	30.1	138	1 RJHU2	retinoic acid-bind
28	213	29.9	137	1 RJHU1	retinoic acid-bind
29	210	29.5	137	1 RJBUA	retinoic acid-bind

30 210 29.5 137 2 A35825 retinoic acid-bind
31 197.5 27.7 133 2 A39818 14k fatty acid-bin
32 196 27.5 139 2 I53298 cellular retinoic
33 192.5 27.0 133 2 A48578 fatty acid-binding
34 187 26.2 135 1 RJRTO retinol-binding pr
35 186 26.1 135 1 RJHUO retinol-binding pr
36 181 25.4 95 2 A61629 retinoic acid-bind
37 181 25.4 134 2 S43470 fatty-acid-binding
38 181 25.4 135 2 S16355 retinol-binding pr
39 180 25.2 134 2 S34717 retinol-binding pr
40 178.5 25.0 134 2 S29600 fatty acid-binding
41 177 24.8 133 2 A44870 fatty acid-binding
42 176 24.7 134 2 A29065 retinol-binding pr
43 173 24.3 134 2 S69360 retinol-binding pr
44 166 23.3 132 2 A44864 fatty acid-binding
45 158 22.2 100 2 S13796 retinoic acid-bind

ALIGNMENTS

RESULT 1

A47497
lipid-binding protein, keratinocyte - mouse
N:Alternate names: lipid-binding protein mall
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 13-Aug-1999
C:Accession: A47497; S36635
R:Krieg, P.; Feil, S.; Fuerstenberger, G.; Bowden, G.T.
J. Biol. Chem. 268, 17362-17369, 1993
A:Title: Tumor-specific overexpression of a novel keratinocyte lipid-binding protein.
A:Reference number: A47497; MUID:93352523; PMID:8349619
A:Accession: A47497
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <R1>
A:Cross-references: EMBL:X70100; NID:g287985; PIDN:CAA49703.1; PID:g287986
C:Superfamily: myelin P2 protein

Query Match 100.0% Score 713; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 7.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLKDEGKWRMLMESHGFEYMKELGVLALRMAAMAKPDCIITCDGNNITVKTESTV 60

Db 1 MASLKDEGKWRMLMESHGFEYMKELGVLALRMAAMAKPDCIITCDGNNITVKTESTV 60

QY 61 KTVFVSCNLGKFXDETTADGRKTETVCTPDGALVHQHQWDGKESTITRKLKDGKMIVEC 120

Db 61 KTVFVSCNLGKFXDETTADGRKTETVCTPDGALVHQHQWDGKESTITRKLKDGKMIVEC 120

QY 121 VMNATCTRVYEVQ 135

Db 121 VMNATCTRVYEVQ 135

RESULT 2

JC2201

fatty acid-binding protein, cutaneous - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Dec-2000

C:Accession: JC2201; JC7377

R:Watanabe, R.; Fujii, H.; Odani, S.; Sakakibara, J.; Yamamoto, A.; Ito, M.; Ono, T.

Biochem. Biophys. Res. Commun. 200, 253-259, 1994

A:Title: Molecular cloning of a cDNA encoding a novel fatty acid-binding protein from

A:Reference number: JC2201; MUID:94220094; PMID:8166694

A:Accession: JC2201

A:Molecule type: mRNA

A:Residues: 1-135 <WAT>

A:Cross-references: GB:S69874; NID:g546419; PIDN:AAB30574.1; PID:g546420

R:Odani, S.; Namba, Y.; Ishii, A.; Ono, T.; Fujii, H.

J. Biochem. 128, 355-361, 2000

A:Title: Disulfide bonds in rat cutaneous fatty acid-binding protein.

A:Reference number: JC7377

A:Contents: Skin

A:Accession: JC7377

A:Molecule type: mRNA

A:Residues: 1-135 <ODA>

C:Comment: This protein is involved in intracellular transport and metabolism of fatty acid

F:22/Binding site: phosphate (Tyr) (covalent) (by insulin receptor/kinase) #status predicted

F:109/Binding site: fatty acid (Arg) #status predicted

C:Genetics:

A:Gene: c-fabp

C:Superfamily: myelin P2 protein

C:Keywords: cutaneous gland; disulfide bond; phosphoprotein; skin

F:22/Binding site: phosphate (Tyr) (covalent) (by insulin receptor/kinase) #status predicted

F:109/Binding site: fatty acid (Arg) #status predicted

Query Match 93.0%; Score 663; DB 2; Length 135;

Best Local Similarity 91.9%; Pred. No. 5e-57; 5; Indels 0; Gaps 0;

Matches 124; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MASLKDLEGKWRMLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTV 60

Db 1 MASLKDLEGKWRMLVESHGFEYMKELGVGLALRKMAAMAKPDCIITLDGNNITVKTESTV 60

Qy 61 KTVFSCNLGKGFDETTADGRKTEVCTFDGALVQHQWDGKESTITRKLKDGKMWVEC 120

Db 61 KTVFSCNLGKGFDETTADGRKTEVCTFDGALVQHQWDGKESTITRKLKDGKMWVEC 120

Qy 121 VMNNAICTRVYKVKQ 135

Db 121 VMNNAICTRVYKVKQ 135

RESULT 3

I56326

fatty acid binding protein homolog - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I56326

R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Celis, J.E.

J. Invest. Dermatol. 99, 299-305, 1992

A:Title: Molecular cloning and expression of a novel keratinocyte protein (psoriasis-ass

ilarity to fatty acid-binding proteins.

A:Reference number: I56326; MUID:92381332; PMID:1512466

A:Accession: I56326

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-135 <RES>

A:Cross-references: GB:M94856; NID:g182353; PIDN:AAA58467.1; PID:g182354

C:Genetics:

A:Gene: PA-FABP

C:Superfamily: myelin P2 protein

Query Match 85.8%; Score 612; DB 2; Length 135;

Best Local Similarity 80.0%; Pred. No. 4.4e-52;

Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MASLKDLEGKWRMLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTV 60

Db 1 MATVQQLGKRWLVDSKGFDEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTL 60

Qy 61 KTVFSCNLGKGFDETTADGRKTEVCTFDGALVQHQWDGKESTITRKLKDGKMWVEC 120

Db 61 KTVFSCNLGKGFDETTADGRKTEVCTFDGALVQHQWDGKESTITRKLKDGKLVVEC 120

Qy 121 VMNNAICTRVYKVKQ 135

Db 121 VMNNAICTRVYKVE 135

RESULT 4

MPRB2

myelin P2 protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999

C:Accession: A28081; A92266; A92372; A03145

R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.

J. Biol. Chem. 263, 8332-8337, 1988

A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.

A:Reference number: A28081; MUID:89228063; PMID:2453513

A:Accession: A28081

A:Molecule type: mRNA

A:Residues: 1-132 <NAR>

A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658

A>Note: translation of Initiator Met is not shown

R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.

J. Biol. Chem. 255, 1058-1063, 1980

A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.

A:Reference number: A92266; MUID:80094496; PMID:7356651

A:Accession: A92266

A:Molecule type: protein

A:Residues: 2-56 <ISI>

R:Ishaque, A.; Hofmann, T.; Eylar, E.H.

J. Biol. Chem. 257, 592-595, 1982

A:Title: The complete amino acid sequence of thr rabbit P2 protein.

A:Reference number: A92372; MUID:82098098; PMID:6172423

A:Accession: A92372

A:Molecule type: protein

A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction o

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/disulfide bonds: #status predicted

Query Match 54.8%; Score 391; DB 1; Length 132;

Best Local Similarity 57.9%; Pred. No. 1e-30; 31; Indels 0; Gaps 0;

Matches 73; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

Qy 9 GKWRMLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVTKTVFSCN 68

Db 7 GTWKLSSSEFDDYMKALGVGLATRLKGLNLAQPNVLIISKKGDIITRTSTFKNTEISFK 66

Qy 69 LGKEDFETADGRKTEVCTFDGALVQHQWDGKESTITRKLKDGKMWECVNNATCT 128

Db 67 LGQEFETADNRKTKSITLTERGALVQVQWDGKETTIRKLKLVGKMKRGVVCT 126

Qy 129 RVYKVK 134

Db 127 RIYKVK 132

RESULT 5

MPHU2

myelin P2 protein [validated] - human

N:Alternate names: peripheral myelin protein 2

C:Species: Homo sapiens (man)

C:Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000

C:Accession: JT0977; A03143; S24224

R:Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human pe

A:Reference number: JT0977; MUID:92068191; PMID:1720307

A:Accession: JT0977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A>Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785; PMID:6183401

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98,'N',100-110,'D',112-132 <SUZ>

```

RESULT 7
JH0407
myelin p2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 13-Aug-1999
C:Accession: JH0407
R:Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.
J. Neurochem. 57, 75-80, 1991
A:Title: Structure of the mouse myelin p2 protein gene.
A:Reference number: JH0407; MUID:91268811; PMID:1711100

```

RESULT 9
S20297
fatty acid-binding protein, hepatic - nurse shark
C:Species: *Ginglymostoma cirratum* (nurse shark)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999
C:Accession: S20297
R:Medzhiradzsky, K.F.; Gibson, B.W.; Kaur, S.; Yu, Z.; Medzhiradzsky, D.; Burlingame, Eur. J. Biochem. 203, 327-339, 1992.
A:Title: The primary structure of fatty-acid-binding protein from nurse shark liver.
A:Reference number: S20297; MUID:92137215; PMID:1735421
A:Accession: S20297
A:Molecule type: protein

A:Residues: 1-132 <MED>

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; liver; phosphoprotein

F:1/Modified site: acetylated amino end (Val) #status experimental

Query Match 51.1%; Score 364; DB 2; Length 132;
Best Local Similarity 53.5%; Pred. No. 4.3e-28;
Matches 68; Conservative 21; Mismatches 38; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

DB 6 GSWKLOKSHNFDYMKELGVLGALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 65

QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVECMNNATCT 128

DB 66 LAEEFDETTADNRKTKTYKLENGKLKLVQTRWDGKSTITRKLKDGKMIIVECMNNATCT 125

QY 129 RYVEK 135

DB 126 RYVREQ 132

RESULT 10

F2HUF

fatty acid-binding protein, adipocyte - human

N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein 4

C:Species: Homo sapiens (man)

C:Date: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999

C:Accession: A33363

R:Baxa, C.A.; Sna, R.S.; Buel, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Boundy

Biochemistry 28, 8683-8690, 1989

A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloning

A:Reference number: A33363; MUID:90105397; PMID:2481498

A:Accession: A33363

A:Molecule type: mRNA

A:Residues: 1-132 <BAX>

A:Cross-references: GB:J02874; NID:gl78346; PIDN:AAA51689.1; PID:gl78347

A:Experimental source: subcutaneous fat

C:Genetics:

A:Gene: GDB:FABP4

A:Cross-references: GDB:128030

A:Map position: lp33-lp32

C:Superfamily: myelin P2 protein

C:Keywords: blocked amino end; lipid binding; phosphoprotein

F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #status

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Query Match 50.8%; Score 362; DB 1; Length 132;
Best Local Similarity 54.4%; Pred. No. 6.7e-28;
Matches 68; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

DB 7 GTWKLVSSENFDDYMKELGVLGALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 66

QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVECMNNATCT 128

DB 67 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVECMNNATCT 126

QY 129 RYVEK 133

DB 127 RYVER 131

RESULT 11

myelin P2

N:Alternate names: adipocyte lipid-binding protein; adipocyte P2 protein

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2000

C:Accession: B25952; PC1249; A24884; A05089; A30810; I49440; I49467

R:Phillips, M.; Djian, P.; Green, H.

J. Biol. Chem. 261, 10821-10827, 1986

A:Title: The nucleotide sequence of three genes participating in the adipose differenc

A:Reference number: A92553; MUID:86278164; PMID:3015943

A:Accession: B25952

A:Molecule type: DNA

A:Residues: 1-132 <PHI>

A:Cross-references: GB:M13385; NID:gl98718; PIDN:AAA39417.1; PID:gl387401

A:Note: the authors translated the codon GTG for residue 111 as Gly

R:Bansal, M.P.; Medina, D.

Biochem. Biophys. Res. Commun. 191, 61-69, 1993

A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gl

A:Reference number: PC1248; MUID:93191717; PMID:8447836

A:Accession: PC1249

A:Molecule type: protein

A:Residues: 25-35; 37-51; 59-88 <BAN>

A:Experimental source: mammary gland

R:Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 3786-3790, 1986

A:Title: Adipocyte P2 gene: Developmental expression and homology of 5'-flanking sequ

A:Reference number: A24884; MUID:86233319; PMID:3520554

A:Accession: A24884

A:Molecule type: DNA

A:Residues: 1-39,'T',41-110,'G',112-132 <HUN>

A:Cross-references: GB:M13264; NID:g200183; PIDN:AAA39870.1; PID:gl387504

A:Note: the authors translated the codon ACC for residue 40 as Ser

R:Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.

Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472, 1984

A:Title: Expression of specific mRNAs during adipose differentiation: identification

A:Reference number: A05089; MUID:84298159; PMID:6208497

A:Accession: A05089

A:Molecule type: mRNA

A:Residues: 1-110,'G',112-132 <BER>

A:Cross-references: GB:K02109; NID:gl98716; PIDN:AAA39416.1; PID:gl293695

R:Matarese, V.; Bernlohr, D.A.

J. Biol. Chem. 263, 14544-14551, 1988

A:Title: Purification of murine adipocyte lipid-binding protein. Characterization as

A:Reference number: A30810; MUID:89008309; PMID:2844775

A:Accession: A30810

A:Molecule type: protein

A:Residues: 2-110,'G',112-132 <MAT>

R:Cook, K.S.; Hunt, C.R.; Spiegelman, B.M.

J. Cell Biol. 100, 514-520, 1985

A:Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcription

A:Reference number: I49440; MUID:85105214; PMID:3968175

A:Accession: I49440

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 11-110,'G',112-132 <RES>

A:Cross-references: GB:M28726; NID:gl91492; PIDN:AAA37112.1; PID:gl91493

R:Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.;

Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988

A:Title: Expression of the differentiation-induced gene for fatty acid-binding protei

A:Reference number: I49467; MUID:88203618; PMID:2452440

A:Accession: I49467

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RE2>

A:Cross-references: GB:M20497; NID:gl91743; PIDN:AAA37188.1; PID:gl91744

A:Experimental source: 3T3-L1 cells

C:Genetics:

C:Superfamily: myelin P2 protein

C:Keywords: lipid binding; phosphoprotein

Query Match 50.1%; Score 357; DB 2; Length 132;
Best Local Similarity 53.6%; Pred. No. 2e-27;
Matches 67; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

DB 7 GTWKLVSSENFDDYMKELGVLGALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 66

QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKSTITRKLKDGKMIIVECMNNATCT 128

Db 67 LGVEFEITADDRKRSIIITLDGSLVQVQKWDGKSTTIKRKEDVDKLVVECVKMGWTST 126
 QY 129 RYVEK 133
 Db 127 RYVER 131

RESULT 12
 A27452
 fatty acid-binding protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Dec-1988 #sequence-revision 15-Dec-1988 #text-change 13-Aug-1999
 C:Accession: A28458; A27452; A23838; A39551; A28197; S02471
 R:Heuckeroth, R.O.; Birkenmeier, E.H.; Levin, M.S.; Gordon, J.I.
 J. Biol. Chem. 262, 9709-9717, 1987
 A:Title: Analysis of the tissue-specific expression, developmental regulation, and linkage
 A:Reference number: A28458; MUID:87250640; PMID:3036869
 A:Accession: A28458
 A:Molecule type: mRNA
 A:Residues: 1-133 <HEU>
 A:Cross-references: GB:J02773; NID:Q204077; PIDN:AAA41136.1; PID:Q204078
 A:Experimental source: cardiac
 R:Clafiey, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.
 Biochemistry 26, 7900-7904, 1987
 A:Title: Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: 1
 A:Reference number: A27452; MUID:88107756; PMID:3427112
 A:Accession: A27452
 A:Molecule type: mRNA
 A:Residues: 1-133 <CLA>
 A:Cross-references: GB:M18034; NID:Q204079; PIDN:AAA41137.1; PID:Q204080
 A:Experimental source: heart
 R:Sacchettini, J.C.; Said, B.; Schulz, H.; Gordon, J.I.
 J. Biol. Chem. 261, 8218-8223, 1986
 A:Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocy
 A:Reference number: A23838; MUID:86250713; PMID:2424895
 A:Accession: A23838
 A:Molecule type: protein
 A:Residues: 1-133 <TEK>
 A:Experimental source: heart
 R:Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.
 J. Biol. Chem. 266, 5963-5972, 1991
 A:Title: Primary structure and cellular distribution of two fatty acid-binding proteins
 A:Reference number: A39551; MUID:91170283; PMID:2005132
 A:Accession: A39551
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 10-69, 'Q', '71-121, 'D', '123-133 <KIM>
 A:Experimental source: kidney
 R:Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.
 J. Biol. Chem. 263, 4182-4185, 1988
 A:Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by 1
 A:Reference number: A28197; MUID:88153733; PMID:3162235
 A:Accession: A28197
 A:Molecule type: protein
 A:Residues: 2-10; 46-53 <GTB>
 R:Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.; Mut
 Eur. J. Biochem. 185, 27-33, 1989
 A:Title: Purification and characterization of a fatty-acid-binding protein from the gast
 A:Reference number: S06478; MUID:90032682; PMID:2806260
 A:Accession: S06478
 A:Molecule type: protein
 A:Residues: 1-133 <KAN>
 A:Experimental source: stomach
 R:Jones, P.D.; Carne, A.; Bass, N.M.; Grigor, M.R.
 Biochem. J. 251, 919-925, 1988
 A:Title: Isolation and characterization of fatty acid binding proteins from mammary tiss
 A:Reference number: S02471; MUID:88326235; PMID:3415652
 A:Accession: S02471
 A:Molecule type: protein
 A:Residues: 16-22; 32-45; 54-59, 'XX', '62-63, 'X', '65-70; 83-93; 97-107; 117-127 <JON>
 A:Experimental source: strain Wistar; mammary

C:Superfamily: myelin p2 protein
 C:Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotei
 F:133/Product: fatty acid-binding protein #status experimental <MAT>
 F:1/Modified site: acetylated amino end (Met) #status predicted

Query Match 47.1%; Score 336; DB 2; Length 133;
 Best Local Similarity 51.2%; Pred. No. 2.2e-25;
 Matches 64; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGYGLALRKMAAKPKDCITCDGNNTITKSTVKTTFVSCN 68
 Db 7 GTWKLVDSKNFDDYMKSLGSGVFATQVAVSMKPTTIIKNGNDITIKTHSTFNTLSFQ 66
 QY 69 LSGKFFETADGRKTTFTVCFQDQALVHQHQWQKSGSTITRKLKDGKMIIVECVNNATCT 128
 Db 67 LGVEFEITADDRKRSVVTLDGKLVQVQKWDGQETTLTRELSDGKLIILTHGNNVST 126
 QY 129 RYVEK 133
 Db 127 RYVEK 131

RESULT 13
 FZHU0
 fatty acid-binding protein, cardiac and skeletal muscle - human
 A:Alternate names: fatty acid-binding protein 3 (FABP3)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1991 #sequence-revision 03-May-1996 #text-change 16-Jul-1999
 C:Accession: S15432; JH0199; S00603; I54275; A27248
 R:Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.
 Biochem. J. 276, 203-207, 1991
 A:Title: Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protei
 A:Reference number: S15432; MUID:91248148; PMID:1710107
 A:Accession: S15432
 A:Molecule type: mRNA; protein
 A:Residues: 1-133 <PEE>
 A:Cross-references: EMBL:X56549; NID:g31292; PIDN:CAA39889.1; PID:g31293
 A:Experimental source: heart muscle; skeletal muscle
 R:Boerchers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.
 Mol. Cell. Biochem. 98, 127-133, 1990
 A:Title: Revision of the amino acid sequence of human heart fatty acid-binding protei
 A:Reference number: JH0199; MUID:91094793; PMID:2266954
 A:Accession: JH0199
 A:Molecule type: protein
 A:Residues: 2-129, 'Q', '131-133 <BOE>
 R:Offner, G.D.; Brecher, P.; Sawilivich, W.B.; Costello, C.E.; Troxler, R.F.
 Biochem. J. 252, 191-198, 1988
 A:Title: Characterization and amino acid sequence of a fatty acid-binding protein fro
 A:Reference number: S00603; MUID:88339792; PMID:3421901
 A:Accession: S00603
 A:Molecule type: protein
 A:Residues: 2-104, 'K', '106-124, 'S', '126-133 <OFF>
 A:Note: submitted to the Protein Sequence Database, May 1988
 R:Zanotti, G.; Scapin, G.; Spadon, P.; Veerkamp, J.H.; Sacchettini, J.C.
 J. Biol. Chem. 267, 18541-18550, 1992
 A:Title: Three-dimensional structure of recombinant human muscle fatty acid-binding p
 A:Reference number: A49251; MUID:92406763; PMID:1526991
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms
 A:Note: recombinant protein expressed in Escherichia coli
 R:Troxler, R.F.; Offner, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Mlunsky, A.; Wyan
 Hum. Genet. 92, 563-566, 1993
 A:Title: Localization of the gene for human heart fatty acid binding protein to chrom
 A:Reference number: I54275; MUID:94085953; PMID:8262516
 A:Accession: I54275
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 15-133 <RES>
 A:Cross-references: GB:S67314; NID:9458861; PIDN:AAB29294.1; PID:9458862
 C:Genetics:
 A:Gene: GDB:FABP3
 A:Cross-references: GDB:128008; OMIM:134651
 A:Map position: lp33-tp32
 C:Superfamily: myelin p2 protein

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:19:37 ; Search time 36 Seconds
(without alignments)
499.690 Million cell updates/sec

Title: US-09-788-074-1

Perfect score: 713

Sequence: 1 MASLKLEKGRMLMESHGFE.....MIVECVMNATCTRYEKVQ 135

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

1:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	100.0	135	AAU08673	Mouse keratinocyte
2	617	86.5	146	ABG60208	Human D17HP poly
3	612	85.8	135	AAR55866	Melanogenic inhibi
4	612	85.8	135	AAU08674	Human keratinocyte
5	603	84.6	158	ABG27577	Novel human diagno
6	599	84.0	135	ABG61772	Novel fatty acid-b
7	535.5	75.1	134	AAU08666	Human NOV10 protein
8	530.5	74.4	163	AAU08665	Human NOV9 protein
9	387.5	54.3	172	AAU10059	Fatty acid-binding
10	372.5	52.2	181	ABG13617	Novel human diagno

11	368	51.6	136	19	AAW40227	Human myelin P2 pr
12	362	50.8	132	21	AAAY90320	Human AFABP protei
13	362	50.8	132	23	ABB08076	Human ap2 protein.
14	359	50.4	132	21	AAAY90319	Mouse AFABP protei
15	356	49.9	136	19	AAW40228	Bovine myelin P2 p
16	333	46.7	133	22	AAG66578	Human MDGI polypep
17	330	46.3	131	12	AAR13559	MDGI active peptid
18	320.5	45.0	134	18	AAW31534	Porcine heart-fatt
19	320	44.9	133	22	AAG66577	Mouse MDGI polypep
20	318	44.6	133	22	AAG66576	Mouse MDGI polypep
21	293	41.1	117	21	AAG03847	Human secreted pro
22	292	41.0	132	18	AAW22408	Human cytostatin I
23	292	41.0	132	19	AAW80949	Amino acid sequenc
24	292	41.0	132	19	AAW81106	Human cytostatin I
25	292	41.0	132	20	AAW82403	Human 14-16 kDa FA
26	282	39.6	132	16	AAR75423	Mouse cellular X b
27	280.5	39.3	131	22	AAG66580	Human cytostatin I
28	280	39.3	132	21	AAG03957	Human secreted pro
29	257.5	36.1	130	22	ABG62690	Drosophila melanog
30	228	32.0	522	22	ABG13615	Novel human diagno
31	219.5	30.8	149	21	AAW58158	Lung cancer associ
32	214.5	30.1	138	14	AAW42211	CRABP-II gene prod
33	214.5	30.1	138	22	AAW76852	Human lung tumour
34	214.5	30.1	138	23	AAU85507	Clone #19122 of lu
35	213	29.9	137	14	AAW42212	CRABP-I gene produ
36	205.5	28.8	132	22	AAU10065	Cytostatin family
37	205.5	28.8	135	22	AAU10066	Cytostatin family
38	205.5	28.8	433	22	ABG27578	Novel human diagno
39	200.5	28.1	117	22	AAU30142	Novel human secret
40	197.5	27.7	133	16	AAR75643	Schistosoma manso
41	196	27.5	82	22	AAG75123	Human colon cancer
42	196	27.5	88	21	AAW58740	Breast and ovarian
43	193	27.1	160	21	AAW43403	Human cancer assoc
44	186	26.1	219	23	ABP41914	Human ovarian anti
45	184	25.8	135	18	AAW30891	Human cytostatin I

ALIGNMENTS

RESULT 1
AAU08673
ID AAU08673 standard; Protein; 135 AA.
XX AAU08673;
XX
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse keratinocyte fatty acid binding protein, Mall.
XX
XX
KW Mouse; Mal 1; keratinocyte fatty acid binding protein; anorectic;
KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
KW dyslipidaemia; atherosclerosis; antisense therapy.
XX
XX Mus musculus.
XX
XX WO200160384-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US05019.
XX
PR 17-FEB-2000; 2000US-0183106.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Hotamisligil GS;
XX
XX WPI: 2001-570550/64.
XX
XX N-PSDB; AAS13246.
XX
XX Reducing the level of circulating free fatty acids in a mammal, useful
XX for treating or preventing obesity, diabetes, dyslipidaemia or

PT atherosclerosis, by administering a keratinocyte lipid binding protein
PT inhibitor
XX
PS Disclosure; Page 2; 27pp; English.
XX
CC The invention relates to reducing the level of circulating free fatty
CC acids in a mammal comprising administering to a mammal a compound that
CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
CC fatty acid binding protein) or Mall activity. The method is useful for
CC reducing the level of circulating free fatty acids in a mammal,
CC particularly in a mammal that is suffering from or at risk of developing
CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
CC useful for diagnosing these diseases. The present sequence is Mouse
CC Mal 1.
XX
SQ Sequence 135 AA:
Query Match 100.0%; Score 713; DB 22; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.6e-74;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLKDLECKWRLMESHGFEYMKELGVGLARKKMAAMAKPDCIITCDGNNITVKTSTV 60
Db 1 MASLKDLECKWRLMESHGFEYMKELGVGLARKKMAAMAKPDCIITCDGNNITVKTSTV 60
QY 61 KTVFSCNLGERKFEDETTADGRKTTVCTFDGALVHQHQWQDGKESTITRKLKDKGMIVEC 120
Db 61 KTVFSCNLGERKFEDETTADGRKTTVCTFDGALVHQHQWQDGKESTITRKLKDKGMIVEC 120
QY 121 VMNNATCTRVYKQV 135
Db 121 VMNNATCTRVYKQV 135
RESULT 2
ABG60208
ID ABG60208 standard; Protein; 146 AA.
XX
AC ABG60208;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human DITHP polypeptide #266.
XX
KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infections; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW thymus.
XX
OS Homo sapiens.
XX
PN WO200220754-A2.
XX
PD 14-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27127.
XX
PR 05-SEP-2000; 2000US-229747P.
PR 05-SEP-2000; 2000US-229748P.
PR 05-SEP-2000; 2000US-229749P.
PR 05-SEP-2000; 2000US-229750P.
PR 05-SEP-2000; 2000US-229751P.
PR 05-SEP-2000; 2000US-230583P.
PR 06-SEP-2000; 2000US-230584P.
PR 06-SEP-2000; 2000US-230514P.
PR 06-SEP-2000; 2000US-230515P.
PR 06-SEP-2000; 2000US-230517P.
PR 06-SEP-2000; 2000US-230518P.
PR 06-SEP-2000; 2000US-230519P.

PR 06-SEP-2000; 2000US-230595P.
PR 06-SEP-2000; 2000US-230597P.
PR 06-SEP-2000; 2000US-230598P.
PR 06-SEP-2000; 2000US-230599P.
PR 06-SEP-2000; 2000US-230610P.
PR 06-SEP-2000; 2000US-230655P.
PR 06-SEP-2000; 2000US-230988P.
PR 07-SEP-2000; 2000US-230951P.
PR 07-SEP-2000; 2000US-231163P.
PR 07-SEP-2000; 2000US-231167P.
XX (INCY-) INCYTE GENOMICS INC.
PA Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
XX Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI; 2002-383054/41.
DR N-PSDB; ABK71797.
XX
PT An isolated polynucleotide useful in diagnostics and therapeutics -
XX
PS Claim 29; Page 679; 686pp; English.
XX
CC The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention.
XX
SQ Sequence 146 AA:
Query Match 86.5%; Score 617; DB 23; Length 146;
Best Local Similarity 86.9%; Pred. No. 2.3e-63;
Matches 119; Conservative 8; Mismatches 8; Indels 2; Gaps 2;
QY 1 MASLKDLECKWRLMESHGFEYMKELGVGLARKKMAAMAKPDCIITCDGNNITVKTSTV 60
Db 6 MASLKDLECKWRLVESHGFEYMKELGVGLARKKMAAMAKPDCIITLDGNNITVKTSTV 65
QY 61 KTVFSCNLGERKFEDETTADGRKTTVCTFDGALVHQHQWQDGKESTITRKLKDKGMIVEC 120
Db 66 KTVFSCNLGERKFEDETTADGRKTTVCTFDGALVHQHQWQDGKESTITRKLKDKGMIVEC 125
QY 121 VMNNA-TCTR-VYEKQV 135
Db 126 VMNCPCTSGMLTKVQ 142
RESULT 3
AAR55866
ID AAR55866 standard; Protein; 135 AA.
XX
AC AAR55866;
XX
DT 07-DEC-1994 (first entry)
XX
DE Melanogenic inhibitor.
XX
KW Melanogenic inhibitor; MI; melanogenesis; melanin; pigment;

KW depigmentation; melanoma.
 XX Homo sapiens.
 OS WO9412534-A.
 XX PD 09-JUN-1994.
 XX PF 16-NOV-1993; 93WO-US11139.
 XX PR 24-NOV-1992; 92US-0980513.
 XX PR 01-SEP-1993; 93US-0115172.
 XX PA (UYCI-) UNIV CINCINNATI.
 XX PI Faroouqui JZ, Nordlund JJ;
 XX DR WPI: 1994-200198/24.
 XX DR N-PSDB; AAQ66842.
 XX PT Prodn. of a protein for inhibiting melanogenesis - useful for
 PT treating hyper-pigmentary diseases, destroying melanoma cells and
 PT for lightening unwanted body hair
 XX PS Disclosure; Page 5; 40pp; English.
 XX CC PCR primers given in AAQ66843-44 were used to amplify RNA from
 CC human skin previously grafted onto nude mice, thereby providing
 CC DNA (AAQ66842) encoding melanogenic inhibitor protein (AAR55866).
 XX SQ Sequence 135 AA;
 Query Match 85.8%; Score 612; DB 15; Length 135;
 Best Local Similarity 80.0%; Pred. No. 7.9e-63;
 Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MASLKDEKRWLMESHGFEYMKELGVGLALRKKMAAMAKPDCIITCDGNNTVKTSTV 60
 Db 1 MATVQLEGRLVDSKGFDEYMKELGVGLALRKKMGAMAKPDCIITCDGNLTIKTESTL 60
 QY 61 KTVFSCNLGKFEETADGRKTETVCTFDGALVQHQWQDGKKESTITRKLKDGKMLVEC 120
 Db 61 KTFQFCTLGERKFEETADGRKTQVCNFTDGLVQHQWQDGKKESTITRKLKDGKMLVEC 120
 QY 121 VMNNTCTRYEYKQV 135
 Db 121 VMNNTCTRYEYKVE 135
 RESULT 4
 AAU08674
 ID AAU08674 standard; Protein; 135 AA.
 AC AAU08674;
 XX DT 18-DEC-2001 (first entry)
 DE Human keratinocyte fatty acid binding protein, Mall.
 XX KW Human; Mal 1; keratinocyte fatty acid binding protein; anorectic;
 KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
 KW dyslipidaemia; atherosclerosis; antilipemic therapy.
 XX OS Homo sapiens.
 XX PN WO200160384-A1.
 XX PD 23-AUG-2001.
 XX PF 16-FEB-2001; 2001WO-US05019.
 XX PR 17-FEB-2000; 2000US-0183106.

PA (HARD) HARVARD COLLEGE.
 XX PI Hotamisliligil GS;
 XX DR WPI: 2001-570550/64.
 XX DR N-PSDB; AAS13247.
 XX PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidaemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor
 XX PS Disclosure; Page 2; 27pp; English.
 XX CC The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
 CC fatty acid binding protein) or Mall activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
 CC useful for diagnosing these diseases. The present sequence is Human
 CC Mal 1.
 XX SQ Sequence 135 AA;
 Query Match 85.8%; Score 612; DB 22; Length 135;
 Best Local Similarity 80.0%; Pred. No. 7.9e-63;
 Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MASLKDEKRWLMESHGFEYMKELGVGLALRKKMAAMAKPDCIITCDGNNTVKTSTV 60
 Db 1 MATVQLEGRLVDSKGFDEYMKELGVGLALRKKMGAMAKPDCIITCDGNLTIKTESTL 60
 QY 61 KTVFSCNLGKFEETADGRKTETVCTFDGALVQHQWQDGKKESTITRKLKDGKMLVEC 120
 Db 61 KTFQFCTLGERKFEETADGRKTQVCNFTDGLVQHQWQDGKKESTITRKLKDGKMLVEC 120
 QY 121 VMNNTCTRYEYKQV 135
 Db 121 VMNNTCTRYEYKVE 135
 RESULT 5
 ABG27577
 ID ABG27577 standard; Protein; 158 AA.
 XX AC ABG27577;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #27568.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 XX DR N-PSDB; AAS91764.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20: SEQ ID No 57936; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABC00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 158 AA;

Query Match 84.6%; Score 603; DB 22; Length 158;
Best Local Similarity 79.3%; Pred. No. 1.1e-61;
Matches 107; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 1 MASLKDLEKWRMLSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
DB 24 MATVQLEGRWRLLVDSKGFDEYMKELGVGLALRKMGAMPKPCIIITCDGKNTIKTESL 83
QY 61 KTVFSCNLGKFEDETTADGRKTETVCTFDGALVQHQWQDGKESTITRKLKDGKLVVEC 120
DB 84 KTFQFSCNLTGDEFEETADGRKTQTVCNFTDGLVQHQWQDGKESTITRKLKDGKLVVEC 143
QY 121 VMNNATCTRYEKVQ 135
DB 144 VMNNVTCTRIYEKVE 158

RESULT 6
ABG61772
ID ABG61772 standard; Protein; 135 AA.

XX ABG61772;

XX 14-AUG-2002 (first entry)

DE Novel fatty acid-binding protein-like protein.

XX Cancer; metabolic disorder; skin disorder; infectious disease; anorexia;
KW behavioral disorder; valve disease; endocrine disorder; heart disorder;
KW blood disorder; anxiety disorder; brain disorder; inflammatory disorder;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic disturbance; obesity; metabolic syndrome X; wasting disorder;
KW gene therapy; transgenic animal; human.

OS Homo sapiens.

XX WO200229058-A2.

XX 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31248.
XX
XX 05-OCT-2000; 2000US-238323P.
PR 05-OCT-2000; 2000US-238325P.
PR 06-OCT-2000; 2000US-238372P.
PR 06-OCT-2000; 2000US-238373P.
PR 06-OCT-2000; 2000US-238379P.
PR 06-OCT-2000; 2000US-238382P.
PR 06-OCT-2000; 2000US-238383P.
PR 06-OCT-2000; 2000US-238384P.
PR 06-OCT-2000; 2000US-238397P.
PR 06-OCT-2000; 2000US-238400P.
PR 06-OCT-2000; 2000US-238401P.
PR 06-OCT-2000; 2000US-238402P.
PR 14-MAR-2001; 2001US-275892P.
PR 08-JUN-2001; 2001US-296860P.
XX
PA (CURA-) CURAGEN CORP.

XX ShmKets RA, Taupier RJ, Burgess CE, Zerhusen BD, Mezes PS;
PI Rastelli L, Malvankar UM, Grosse WM, Alsobrook JP, Lepley DM;
PI Spytek KA, Li L, Edinger S, Gerlach V, Ellerman K, Macdougall J;
PI Gunther E, Millet I, Stone D, Smithson G, Szekeres ES;
XX
DR WPI; 2002-444103/47.
XX N-PSDB; ABK92039.

XX Novel isolated polypeptide, designated NOVX, useful for treating or
PT preventing cancer, diabetes, obesity, dyslipidaemia, anorexia, and
PT metabolic, neurodegenerative, immune and hematopoietic disorders -
XX
PS Claim 1; Page 42; 316pp; English.

XX The invention describes an isolated polypeptide (I), useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease. (I), the polynucleotide encoding it (II) and an antibody
CC (III) to (I) are useful for treating or preventing cancer, metabolic
CC disorders, skin diseases, infectious diseases, anorexia, behavioral
CC disorders, valve diseases, endocrine disorders, heart and blood
CC disorders, anxiety disorders, brain disorders, inflammatory disorders,
CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, and the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases. (I), (II) or (III) are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g., diagnostic assays and prognostic assays), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) is
CC useful as immunogen to produce antibodies immunospecific for (I), to
CC screen for potential agonist and antagonist compounds, and as bait
CC protein in a two-hybrid or three-hybrid assay. (II) is useful in gene
CC therapy, to express (I), to detect (I) mRNA or a genetic lesion in a (I)
CC gene, and to modulate activity of (I). A cell containing a vector
CC expressing (I) is useful for producing non-human transgenic animals.
CC This is the amino acid sequence of a novel human polypeptide described
CC in the invention.

XX Sequence 135 AA;

Query Match 84.0%; Score 599; DB 23; Length 135;
Best Local Similarity 77.8%; Pred. No. 2.5e-61;
Matches 105; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

QY 1 MASLKDLEKWRMLSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTSTV 60
DB 1 MATVQLEGRWRLLVDSKGFDEYMKELGVGLALRKMGAMPKPCIIITCDGNNITVKTSTL 60
QY 61 KTVFSCNLGKFEDETTADGRKTETVCTFDGALVQHQWQDGKESTITRKLKDGKLVVEC 120
DB 61 KTFQFSCNLTGDEFEETADGRKTQTVCNFTDGLVQHQWQDGKESTITRKLKDGKLVVEC 120
QY 121 VMNNATCTRYEKVQ 135
XX
XX

Db 121 VMNNVCTRIYEKVE 135

RESULT 7

AAU08666

ID AAU08666 standard; Protein: 134 AA.

XX AC AAU08666;

XX DT 18-DEC-2001 (first entry)

XX DE Human NOV10 protein.

XX KW Human; NOV10; cytostatic; nootropic; neuroprotective; vulnerary;

XX KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;

XX KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;

XX KW antiatherosclerotic; dermatological; cancer; neurological disorder;

XX KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;

XX KW immune disorder; autoimmune disease; respiratory disorder;

XX KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;

XX KW cell growth regulation disorder; lesional psoriatic skin;

XX KW atherosclerosis; abdominal aortic aneurysm.

XX OS Homo sapiens.

XX PN WO200168851-A2.

XX PD 20-SEP-2001.

XX PF 12-MAR-2001; 2001WO-US07735.

XX PR 10-MAR-2000; 2000US-0188277.

XX PR 10-MAR-2000; 2000US-0188316.

XX PR 14-MAR-2000; 2000US-0189139.

XX PR 14-MAR-2000; 2000US-0189140.

XX PR 17-MAR-2000; 2000US-0190231.

XX PR 17-MAR-2000; 2000US-0190401.

XX FA (CURA-) CURAGEN CORP.

XX PI Padigar M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;

XX PI Majumder K, Li L;

XX XX WPI; 2001-570869/64.

XX DR N-PSDB; AAS13344.

XX PT Novel polypeptides and nucleic acids homologous to members of collagen,

XX PT potassium channel, tufelin family of proteins for diagnosing, treating

XX PT cancer, atherosclerosis, neurological, skin and enamel defect disorders

XX PT (NOV11). NOVX polypeptide is also useful for identifying an agent that

PS Claim 1; Page 37; 128pp; English.

XX The invention relates to isolated NOVX (NOVX1-11) polypeptides and

XX the polynucleotides that encode them. NOVX polypeptides, polynucleotides

XX and anti-NOVX antibodies are useful for treating or preventing a

XX pathology associated with NOVX polypeptide in humans and for treating a

XX syndrome associated with human disease e.g. disorders characterised by

XX altered cell motility, proliferation and migration e.g. cancer,

XX angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.

XX episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's

XX disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,

XX asthma, hypertension and seizure (NOV4), enamel defects, such as

XX amelogenesis imperfecta and disorders involving enamel defects,

XX including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic

XX neurological disorders, e.g. paraneoplastic limbic of brain-stem

XX encephalitis occurring during testicular cancer, diabetes, reproductive

XX health, metabolic and endocrine disorders, gastrointestinal disorders,

XX immune disorders and autoimmune diseases, respiratory disorders, bone

XX disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell

XX growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and

XX atherosclerosis, abdominal aortic aneurysm and neurological disorders

XX (NOV11). NOVX polypeptide is also useful for identifying an agent that

CC binds to it and a cell expressing NOVX polypeptide is useful for

CC identifying a therapeutic agent for use in treatment of a NOVX related

CC pathology. The antibodies and a polypeptide having 95% sequence identity

CC to NOVX polypeptide are useful for treating a pathological state in a

CC mammal. The present sequence represents NOV10, a possible epidermal

CC fatty acid-binding protein family member.

XX SQ Sequence 134 AA;

Query Match 75.1%; Score 535.5; DB 22; Length 134;

Best Local Similarity 71.1%; Pred. No. 5.7e-54;

Matches 96; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MASLKDEGKWLKMGHGFEEYMKELGVLALRKMAAMAKPCIIITCGNNITVTESTV 60

Db 1 MATVOQLEGRWLEADSKGFDAYMKKLGVLISLRNMGAMAKPCIIITCGKNTIKTESTL 60

Qy 61 KTVFPCNLGKGFDETTADGRKTEVCTFQDGLVHQWQDCKESTITRKLKDKRMIVEC 120

Db 61 KTQFSCFTLGEKFEFGTTAVGRKTQTVCSFTDGLVPHQMDGKENTITRKLKDKAS-VVDC 119

Qy 121 VMNNATCTRVYEKVVQ 135

Db 120 VMNNVCTRIYEKVE 134

RESULT 8

AAU08665

ID AAU08665 standard; Protein: 163 AA.

XX AC AAU08665;

XX DT 18-DEC-2001 (first entry)

XX DE Human NOV9 protein.

XX KW Human; NOV9; cytostatic; nootropic; neuroprotective; vulnerary;

XX KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;

XX KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;

XX KW antiatherosclerotic; dermatological; cancer; neurological disorder;

XX KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;

XX KW immune disorder; autoimmune disease; respiratory disorder;

XX KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;

XX KW cell growth regulation disorder; lesional psoriatic skin;

XX KW atherosclerosis; abdominal aortic aneurysm.

XX OS Homo sapiens.

XX PN WO200168851-A2.

XX PD 20-SEP-2001.

XX PF 12-MAR-2001; 2001WO-US07735.

XX PR 10-MAR-2000; 2000US-0188277.

XX PR 10-MAR-2000; 2000US-0188316.

XX PR 14-MAR-2000; 2000US-0189139.

XX PR 14-MAR-2000; 2000US-0189140.

XX PR 17-MAR-2000; 2000US-0190231.

XX PR 17-MAR-2000; 2000US-0190401.

XX FA (CURA-) CURAGEN CORP.

XX PI Padigar M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;

XX PI Majumder K, Li L;

XX XX WPI; 2001-570869/64.

XX DR N-PSDB; AAS13344.

XX PT Novel polypeptides and nucleic acids homologous to members of collagen,

XX PT potassium channel, tufelin family of proteins for diagnosing, treating

XX PT cancer, atherosclerosis, neurological, skin and enamel defect disorders

XX PT (NOV11). NOVX polypeptide is also useful for identifying an agent that


```

Db 67 LGQEFETADNRKTSIVTLQSGSLNQVRWDGKRETTIKRKLVLNGKMAVECKMGVCT 126
QY 129 RVEK 132
Db 127 RYD 130

RESULT 12
AAAY90320
ID AAY90320 standard; Protein; 132 AA.
XX
AC AAY90320;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human AFABP protein sequence.
XX
KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
KW serum cholesterol; therapy; human.
XX
OS Homo sapiens.
XX
PN WO200047734-A1.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US03560.
XX
PR 12-FEB-1999; 99US-0119880.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Lee M, Perrella MA, Hotamisligil GS;
XX
WPI: 2000-506094/45.
DR N-PSDB; AAA37717.
XX
Reducing expression of adipocyte fatty acid binding protein through
PT administration of a compound is used to inhibit formation of an
PT atherosclerotic lesion.
XX
PS Disclosure: Page 14; 43pp; English.
XX
This sequence represents the human AFABP (adipocyte fatty
CC acid binding protein) protein sequence. The invention relates to a method
CC for inhibiting formation of an atherosclerotic lesion comprising
CC administering to a mammal a compound that reduces expression of adipocyte
CC fatty acid binding protein (AFABP). The method is used to inhibit
CC formation of atherosclerotic lesions. The method is used to identify
CC compounds which can be used to inhibit formation of atherosclerotic
CC lesions through inhibition of AFABP binding to an intracellular ligand
CC in a macrophage or adipocyte, inhibition of development of an
CC atherosclerotic lesion, inhibition of a macrophage differentiating into
CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity
CC may be inhibited to treat atherosclerosis or to treat individuals at risk
CC of developing atherosclerosis. Inhibiting AFABP expression or activity
CC reduces the development of atherosclerotic lesions despite a high level
CC of serum cholesterol.
XX
SQ Sequence 132 AA;
Query Match 50.8%; Score 362; DB 21; Length 132;
Best Local Similarity 54.4%; Pred. No. 7e-34;
Matches 68; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEEYKELGVGLALRKMAAMAKPDCIITCDGNIIIVKTESTVKTTFVSCN 68
Db 7 GTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFI 66
QY 69 LGKEFDETTADGRKTTCTVTFODGALVHQWQDGGKSTITRKLKDGKMLVECMNNATCT 128

```

```

Db 67 LGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRRKREDDKLVEECVMKGVST 126
QY 129 RVEK 133
Db 127 RYER 131

RESULT 13
ABB08076
ID ABB08076 standard; protein; 132 AA.
XX
AC ABB08076;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human ap2 protein.
XX
KW ap2; antiarteriosclerotic; cardiant; cerebroprotective; antianginal;
KW cytosolic protein; adipocyte; HMG CoA reductase; pravastatin; human.
XX
OS Homo sapiens.
XX
PN US2002035064-A1.
XX
PD 21-MAR-2002.
XX
PF 13-JUL-2001; 2001US-0905235.
XX
PR 17-SEP-1998; 98US-100677P.
XX
PR 07-SEP-1999; 99US-0390275.
XX
PA (ROBL/) ROBL-J A.
PA (PARK/) PARKER R A.
PA (BILL/) BILLER S A.
PA (JAMI/) JAMIL H.
PA (JACO/) JACOBSON B L.
PA (KODU/) KODUKULA K.
XX
PI Robl JA, Parker RA, Biller SA, Jamil H, Jacobson BL, Kodukula K;
XX
WPI: 2002-470589/50.
XX
Method useful for treatment of e.g. atherosclerosis, myocardial
PT infarction, angina involves administering ap2 inhibitor e.g.
PT (2'-(4,5-diphenyl-oxazol-2-yl)-biphenyl-3-yloxy)-acetic acid -
XX
PS Disclosure: Page 16; 26pp; English.
XX
The invention relates to the treatment of atherosclerosis which involves
CC administering an ap2 inhibitor or a combination of an ap2 inhibitor and
CC another type antiatherosclerotic agent, for example, an HMG CoA reductase
CC inhibitor such as pravastatin. The method is used for treating
CC atherosclerosis; for preventing, inhibiting or reducing risk of
CC cardiovascular disorders e.g. cardiac and/or cerebral ischaemia,
CC myocardial infarction, angina, peripheral vascular disease and stroke.
CC The present sequence represents the amino acid sequence of human ap2
CC protein, a cytosolic protein present in adipocytes.
XX
SQ Sequence 132 AA;
Query Match 50.8%; Score 362; DB 23; Length 132;
Best Local Similarity 54.4%; Pred. No. 7e-34;
Matches 68; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEEYKELGVGLALRKMAAMAKPDCIITCDGNIIIVKTESTVKTTFVSCN 68
Db 7 GTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFI 66
QY 69 LGKEFDETTADGRKTTCTVTFODGALVHQWQDGGKSTITRKLKDGKMLVECMNNATCT 128
Db 67 LGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRRKREDDKLVEECVMKGVST 126
QY 129 RYER 133

```


Db 127 RYER 131
|||||

RESULT 14
AA90319
ID AAY90319 standard; Protein; 132 AA.

XX AAY90319;

XX 22-NOV-2000 (first entry)

XX Mouse AFABP protein sequence.

XX AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
XX lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
KW serum cholesterol; therapy; mouse.

OS Mus sp.

XX WO200047734-A1.

PN 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03560.

XX 12-FEB-1999; 99US-0119880.

XX (HARD) HARVARD COLLEGE.

XX Lee M, Perrella MA, Hotamisligil GS;

XX WPI; 2000-506094/45.

DR N-PSDB; AAA37716.

XX Reducing expression of adipocyte fatty acid binding protein through
XX administration of a compound is used to inhibit formation of an
XX atherosclerotic lesion

PS Disclosure: Page 14; 43pp; English.

XX This sequence represents the mouse AFABP (adipocyte fatty
XX acid binding protein) protein sequence. The invention relates to a method
XX for inhibiting formation of an atherosclerotic lesion comprising
XX administering to a mammal a compound that reduces expression of adipocyte
XX fatty acid binding protein (AFABP). The method is used to inhibit
XX formation of atherosclerotic lesions. The method is used to identify
XX compounds which can be used to inhibit formation of atherosclerotic
XX lesions through inhibition of AFABP binding to an intracellular ligand
XX in a macrophage or adipocyte, inhibition of development of an
XX atherosclerotic lesion, inhibition of a macrophage differentiating into
XX a foam cell or inhibition of AFABP expression in a cell. AFABP activity
XX may be inhibited to treat atherosclerosis or to treat individuals at risk
XX of developing atherosclerosis. Inhibiting AFABP expression or activity
XX reduces the development of atherosclerotic lesions despite a high level
XX of serum cholesterol.

SQ Sequence 132 AA;

Query Match 50.4%; Score 359; DB 21; Length 132;
Best Local Similarity 53.6%; Pred. No. 1.6e-33;
Matches 67; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFBEYMKELGVLALRKKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

Db 7 GTWKLVSSENFDDYMKVEGVGATRKVAGMKNPMLIISVNGDLVTRSESTFKNTEISFK 66

QY 69 LGKEFDETTADGRKTTCTFODGALVQHQWDGKESTITRKLKDGKMIKVECMNNATCT 128

Db 67 LGVFEIDTADGRKVKSIITLDGALVQVQKWDGKSTTIKRRDGLKLVVECMKGVGTST 126

QY 129 RYER 133

|||||

Db 127 RYER 131

RESULT 15

AAW40228

ID AAW40228 standard; Protein; 136 AA.

XX AAW40228;

XX 26-JUN-1998 (first entry)

XX Bovine myelin P2 protein.

XX Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW Guillian-Barre syndrome; vasculitis; nerve inflammation;
KW gammopathy.

OS Bos taurus.

XX WO9803647-A2.

PN 29-JAN-1998.

XX 18-JUL-1997; 97WO-DE01535.

XX 18-JUL-1996; 96DE-1029095.

XX (GOLD/) GOLD R.

PA (WEIS/) WEISHAUPT A.

XX Gold R, Weishaupt A;

XX WPI; 1998-120772/11.

XX Recombinant myelin proteins for treating T-cell mediated disease of
XX peripheral nervous system - by high dose antigen therapy, causing
XX apoptosis in T cells, for treating e.g. polyneuritis or
XX Guillian-Barre syndrome

PS Disclosure: Fig 4; 14pp; German.

XX The present sequence is the bovine myelin P2 protein, which can
XX be used to treat T-cell mediated diseases of the peripheral nervous
XX system, especially chronic-inflammatory polyneuritis,
XX Guillian-Barre syndrome, vasculitis and nerve inflammation in cases
XX of gammopathy.

SQ Sequence 136 AA;

Query Match 49.9%; Score 356; DB 19; Length 136;
Best Local Similarity 54.0%; Pred. No. 3.6e-33;
Matches 67; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMSHGFBEYMKELGVLALRKKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68

Db 7 GTWKLVSSENFDDYMKVEGVGATRKVAGMKNPMLIISVNGDLVTRSESTFKNTEISFK 66

QY 69 LGKEFDETTADGRKTTCTFODGALVQHQWDGKESTITRKLKDGKMIKVECMNNATCT 128

Db 67 LGQEFDETTADNRKTKSTVTLARGSLNQVQKWDGNETTIKRLKLVNGKVMVECKMKDVVCT 126

QY 129 RYVE 132

Db 127 RYVD 130

Search completed: November 25, 2002, 10:23:46
Job time : 37 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:22:32 ; Search time 31 Seconds
(without alignments)
897.302 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKDLGKRLMESHCFFE.....MIVECVMNATCTRYEKVQ 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL-21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	53.7	132	13 Q90X55	Q90X55 gallus gall
2	371	52.0	132	13 Q8QHA8	Q8QHA8 anser anser
3	351	49.2	132	11 Q3DAK4	Q3DAK4 mus musculus
4	333	46.7	150	11 Q9R290	Q9R290 rattus norv
5	331	46.4	113	6 Q9XSG4	Q9XSG4 oryctolagus
6	331	46.4	132	13 Q90W92	Q90W92 fundulus he
7	329	46.1	132	11 Q9DAL2	Q9DAL2 mus musculus
8	317	44.5	125	6 Q9XSI5	Q9XSI5 equus caball
9	309.5	43.4	134	13 Q57691	Q57691 cryodracro a
10	308.5	43.3	134	13 Q57665	Q57665 gobionototh
11	308	43.2	135	13 Q91896	Q91896 anguilla ja
12	307.5	43.1	134	13 Q57666	Q57666 paracheaenic
13	305.5	42.8	134	13 Q57663	Q57663 notiothenia
14	301	42.2	132	13 Q918N9	Q918N9 brachydanio
15	299	41.9	133	13 Q8UVC7	Q8UVC7 brachydanio
16	289	40.5	136	5 Q8WR15	Q8WR15 metapenaeus

ALIGNMENTS

RESULT 1

Q90X55 PRELIMINARY; PRT: 132 AA.

AC Q90X55; Q90X56;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Adipocyte fatty acid binding protein.
GN AFAP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Wang Q., Ao J., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Study on chicken AFAP gene as candidate gene for fatness trait."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene in chicken."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene in chicken."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF432507; AAL30744.2; -
DR EMBL: AF432506; AAL30743.1; -
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocin_cytfABP.
DR Pfam: PF00061; Lipocalin; 1.

17	283	39.7	99	6	097675	097675 sus scrofa
18	283	39.7	133	13	057668	057668 cryodracro a
19	282	39.6	133	13	057667	057667 chaenoccephala
20	282	39.6	133	13	057670	057670 gobionototh
21	281	39.4	133	13	057669	057669 notiothenia
22	274	38.4	166	4	Q9H047	Q9H047 homo sapien
23	262	36.7	152	5	Q965W1	Q965W1 caenorhabdl
24	257.5	36.1	130	5	Q9VGM2	Q9VGM2 drosophila
25	254	35.6	111	13	Q90ZG6	Q90ZG6 brachydanio
26	245	34.4	86	13	Q8UWD3	Q8UWD3 anser anser
27	239.5	33.6	100	13	057664	057664 rhigophilla
28	235.5	33.0	137	5	002323	002323 caenorhabdl
29	234.5	32.9	136	5	001814	001814 caenorhabdl
30	234	32.8	97	11	Q9QV90	Q9QV90 mus sp. lmg
31	233.5	32.7	135	5	001812	001812 caenorhabdl
32	224	31.4	132	5	061236	061236 manduca sex
33	217.5	30.5	132	5	026517	026517 schistosoma
34	213.5	29.9	133	5	Q9BMK1	Q9BMK1 echinococcu
35	213.5	29.9	133	5	Q9BLX5	Q9BLX5 echinococcu
36	209.5	29.4	132	5	Q9BME8	Q9BME8 schistosoma
37	208.5	29.2	132	5	Q9UIG6	Q9UIG6 fasciola he
38	208.5	29.2	132	5	045035	045035 schistosoma
39	205.5	28.8	133	5	Q967X3	Q967X3 echinococcu
40	199.5	28.0	147	13	Q9PSA5	Q9PSA5 xenopus lae
41	197.5	27.7	133	5	Q9BMK2	Q9BMK2 echinococcu
42	196.5	27.6	133	5	Q9BMK3	Q9BMK3 echinococcu
43	191.5	26.9	133	5	Q8T5U9	Q8T5U9 schistosoma
44	178.5	25.0	120	5	045036	045036 schistosoma
45	178	25.0	98	5	Q8T5U8	Q8T5U8 schistosoma

```
DR PROSITE; PS00214; FAPB; UNKNOWN_1.
SQ SEQUENCE 132 AA; 14894 MW; 4F5905FAB8DA268B CRC64;

Query Match          53.7%; Score 383; DB 13; Length 132;
Best Local Similarity 57.6%; Pred. No. 4.5e-31;
Matches 72; Conservative 19; Mismatches 34; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 7 GTWKLSSSENFEDYMKELGVGFATRKMGVAKPNLTISINGDVITIRSESTFKNTEISFK 66
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 69 LGKEFDETTADGRKTETVCTFQDQALVQHQWMDGKESTITRKLDGKMIVECVNNATCT 128
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 67 LGKEFDETTADGRKTETVCTFQDQALVQHQWMDGKESTITRKLDGKMIVECVNNATCT 126
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 129 RVYEK 133
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 127 RVYER 131
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2
Q8QHA8 PRELIMINARY; PRT; 132 AA.
AC Q8QHA8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Adipocyte fatty acid-binding protein.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Ao J., Wang Q., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid-binding protein gene
   in goose.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF473610; AAL79836.1; -.
SQ SEQUENCE 132 AA; 14772 MW; 5FD4817B02DA31BB CRC64;

Query Match          52.0%; Score 371; DB 13; Length 132;
Best Local Similarity 56.8%; Pred. No. 7.3e-30;
Matches 71; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVLGALRKMAAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 7 GTWKLSSSENFEDYMKELGVGFATRKMGVAKPNLTISINGDVITIRSESTFKNTEISFK 66
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 69 LGKEFDETTADGRKTETVCTFQDQALVQHQWMDGKESTITRKLDGKMIVECVNNATCT 128
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 67 LGKEFDETTADGRKTETVCTFQDQALVQHQWMDGKESTITRKLDGKMIVECVNNATCT 126
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 129 RVYEK 133
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 127 RVYER 131
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3
Q9DAK4 PRELIMINARY; PRT; 132 AA.
AC Q9DAK4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 1700008G05Rik protein.
GN 1700008G05Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005765; BAB24227.1; -.
DR HSSP; P02690; 1PMP.
DR MGD; MGI:1922747; 1700008G05Rik.
DR InterPro; IPR000463; Fatty_acid_BP
DR InterPro; IPR000566; Lipocln_cycFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 132 AA; 14758 MW; 7A20C53780845F61 CRC64;

Query Match          49.2%; Score 351; DB 11; Length 132;
Best Local Similarity 51.6%; Pred. No. 7.6e-28;
Matches 66; Conservative 22; Mismatches 40; Indels 0; Gaps 0;

QY 7 LEQKWLMSHGFEYMKELGVLGALRKMAAMAKPDCIITCDGNNTVKTSTVKTTFVS 66
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 5 LQGTWKSVCNDNFENYMKELGVGRASRLGCLAKPTVISTDGLTIKTSIFKNKEIS 64
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 67 CNLGEKFEDETTADGRKTETVCTFQDQALVQHQWMDGKESTITRKLDGKMIVECVNNAT 126
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 65 FKLGEEFEETTPSGRSKSTVILDNDLSLVQVQWMDGKEATICRRLVDGKMVSVAVNNVT 124
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 127 CTRVYEK 134
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 125 CTRTYORV 132
   I::: I ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
Q9R290 PRELIMINARY; PRT; 150 AA.
AC Q9R290;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Adipocyte lipid-binding protein.
GN ALBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=ADIPOSE TISSUE;
RX MEDLINE=99254074; PubMed=10318917;
RA Shen W.-J., Sridhar K., Bernlohr D.A., Kraemer F.B.;
RT "Interaction of rat hormone-sensitive lipase with adipocyte lipid-
   binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).
DR EMBL; AF144756; AAD37371.1; -.
DR HSSP; P04117; 1LID.
DR InterPro; IPR000463; Fatty_acid_BP.
```

```
DR InterPro: IPR000566; Lipocln_cytfABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 150 AA: 16468 MW; 9D214AB610D0C54E CRC64;

Query Match 46.7%; Score 333; DB 11; Length 150;
Best Local Similarity 48.8%; Pred. No. 5.8e-26;
Matches 61; Conservative 24; Mismatches 40; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVGLALRMAAMAKPCDIITCDGNNITVKTESTVKTTFVSCN 68
   |::|: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 7 GTWLVSSNFDDYMKELGVGFATRKVAGMAKPNLIISVEGLVIRSESTFKNTEISFK 66

QY 69 LGEKFEDETTADGRKTETVCTFODGALVHQHQWGDKESTITRKLDGKMIVECMNNATCT 128
   |::|: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 67 LGVEFEITPDGRKVKSIITLDGGVLVHVQKWDGKSTTIKRKXDGDKLVVECMKGVGTST 126

QY 129 RYVEK 133
Db 127 RYXR 131

RESULT 5
Q9XSG4 PRELIMINARY; PRT; 113 AA.
ID Q9XSG4
AC Q9XSG4;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Adipocyte lipid-binding protein (Fragment).
GN AP2...
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=URINARY BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
RT "Expression of ap2 gene in transitional epithelium of rabbit
   bladder.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF136241; AAD32209.1; -.
DR HSSP: P04117; ILID.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytfABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA: 12536 MW; 4C19A538EC897F4F CRC64;

Query Match 46.4%; Score 331; DB 6; Length 113;
Best Local Similarity 55.4%; Pred. No. 6.6e-26;
Matches 62; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 11 WRLMSHGFEYMKELGVGLALRMAAMAKPCDIITCDGNNITVKTESTVKTTFVSCNIG 70
   |::|: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 2 WKLVSSENFDDYMKELGVGFATRKVAGMAKPNLIISVNGDVITIKSESTFKNTEISFKLG 61

QY 71 EKFEDETTADGRKTETVCTFODGALVHQHQWGDKESTITRKLDGKMIVECMV 122
   |::|: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 QBEFEVTTADGRKSIITLDGGALVQVQKWDGKSTTIKRKRGDKLVVECMV 113

RESULT 6
Q90W92 PRELIMINARY; PRT; 132 AA.
ID Q90W92
AC Q90W92;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
```

```
DE Heart-type fatty acid-binding protein.
OS H-FABP.
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Bain L.J., Peterson J.S.K., Maples N.L.;
RT "cDNA Cloning, Sequencing, and Expression of a Heart-Type Fatty Acid-
   Binding Protein in the Mummichog (Fundulus heteroclitus).";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY034789; AAK61550.1; -.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytfABP.
DR Pfam: PF00061; lipocalin; 1.
DR PROSITE: PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 132 AA: 14756 MW; D2D842CD52795AAB CRC64;

Query Match 46.4%; Score 331; DB 13; Length 132;
Best Local Similarity 49.6%; Pred. No. 7.9e-26;
Matches 62; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 9 GKWLMSHGFEYMKELGVGLALRMAAMAKPCDIITCDGNNITVKTESTVKTTFVSCN 68
   |::|: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 7 GTWLVSSNFDDYMKELGVGFATRKVGNLTPTTITCVDGKVTVKSTIKNTEISFK 66

QY 69 LGEKFEDETTADGRKTETVCTFODGALVHQHQWGDKESTITRKLDGKMIVECMNNATCT 128
   |::|: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 67 LGEFEDETTADGRKSLVTIEDGKLVHVQKWDGKSTTLVREVDGKNTLTLTIGVWSK 126

QY 129 RYVEK 133
Db 127 RHYEK 131

RESULT 7
Q9DAL2 PRELIMINARY; PRT; 132 AA.
ID Q9DAL2
AC Q9DAL2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 1700007P10RIK protein.
GN 1700007P10RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
```

```

RESULT 9
O57691 PRELIMINARY; PRT; 134 AA.
ID AC O57691;
AC O57691;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Cryodrac antarcticus (Crocodile icefish), and
OS Chaenoccephalus acroatus (white crocodile fish).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
OC Notothenioidae; Channichthyidae; Cryodrac.
OX NCBI_TaxID=36192; 36190;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Winnard P.,
RA Small D.J., Hatch H., Sidell B.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92443; AAC60351.1; -
DR EMBL; U92442; AAC60350.1; -
DR HSSP; P10790; 1BW.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000586; Lipocin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15138 MW; D4CBFC689147A98 CRC64;

Query Match 43.4%; Score 309.5; DB 13; Length 134;
Best Local Similarity 43.5%; Pred. No. 1.2e-23;
Matches 54; Conservative 29; Mismatches 40; Indels 1; Gaps

QY 9 GKRLMESHGFEYMKELGVGLALRKMAAMKPDCIITCDGNN-ITVKTESTVKTTVFSC 67
DB 7 GTWKMTSSDNFDYMKAGVGFATRGVNTKPNLVSVDDQGFVCLKSQSTFKTTEIKF 66

QY 68 NLGKEFDETTADGKKTETVCTFODGALVQHQQDGRKESTITRKLKDGKMWCEVMNATC 127
DB 67 KLEPPETTTADDRKTKTVVTVLENGKLKVKQSDGKTNIERIEDGKLVAKKMGDVIA 126

QY 128 TRVY 131
DB 127 VRVY 130

RESULT 10
O57665 PRELIMINARY; PRT; 134 AA.
ID AC O57665;
AC O57665;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Gobionotothen gibberifrons (Humped rockcod).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Gobionotothen.
OX NCBI_TaxID=36202;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RA MEDLINE=98129752; PubMed=9461533;
RL "Two distinct types of fatty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).

```

```

DR EMBL: U92446; AAC60354.1; -.
DR HSSP: P10790; IHWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipoclin_cytfABP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FAPB; 1.
SQ SEQUENCE 134 AA; 15152 MW; D16BCFD514A2B268 CRC64;

Query Match 43.3%; Score 308.5; DB 13; Length 134;
Best Local Similarity 43.5%; Pred. No. 1.5e-23;
Matches 54; Conservative 28; Mismatches 41; Indels 1; Gaps

Qy 9 GKWRLEMSHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNN-ITVKTESTVKTTFVESC 67
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 7 GTWKMSISDNFDDYMKYKAIGVGFATRQVGNRTKPNLVSVDDQGFVCLKQSSTFKTTEIKF 66

Qy 68 NLGKEFDETTAGDGRKTEVCTFDGALVQHQHDGKRESTITRKLKDGKMLVECVMMNATC 127
| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 67 KLNPEFFETADDRKTRFVTVLTKGLVKQSDGKETNIERIEIDGKLVAKCIMGDVIA 126

Qy 128 TRVY 131
| |
Db 127 VRTY 130

RESULT 11
Q9I896 PRELIMINARY; PRT: 135 AA.
AC Q9I896:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Heart fatty acid binding protein.
GN H-FABP.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN 11
RN 12
RN 13
RN 14
RN 15
RN 16
RN 17
RN 18
RN 19
RN 20
RN 21
RN 22
RN 23
RN 24
RN 25
RN 26
RN 27
RN 28
RN 29
RN 30
RN 31
RN 32
RN 33
RN 34
RN 35
RN 36
RN 37
RN 38
RN 39
RN 40
RN 41
RN 42
RN 43
RN 44
RN 45
RN 46
RN 47
RN 48
RN 49
RN 50
RN 51
RN 52
RN 53
RN 54
RN 55
RN 56
RN 57
RN 58
RN 59
RN 60
RN 61
RN 62
RN 63
RN 64
RN 65
RN 66
RN 67
RN 68
RN 69
RN 70
RN 71
RN 72
RN 73
RN 74
RN 75
RN 76
RN 77
RN 78
RN 79
RN 80
RN 81
RN 82
RN 83
RN 84
RN 85
RN 86
RN 87
RN 88
RN 89
RN 90
RN 91
RN 92
RN 93
RN 94
RN 95
RN 96
RN 97
RN 98
RN 99
RN 100
RN 101
RN 102
RN 103
RN 104
RN 105
RN 106
RN 107
RN 108
RN 109
RN 110
RN 111
RN 112
RN 113
RN 114
RN 115
RN 116
RN 117
RN 118
RN 119
RN 120
RN 121
RN 122
RN 123
RN 124
RN 125
RN 126
RN 127
RN 128
RN 129
RN 130
RN 131
RN 132
RN 133
RN 134
RN 135
RN 136
RN 137
RN 138
RN 139
RN 140
RN 141
RN 142
RN 143
RN 144
RN 145
RN 146
RN 147
RN 148
RN 149
RN 150
RN 151
RN 152
RN 153
RN 154
RN 155
RN 156
RN 157
RN 158
RN 159
RN 160
RN 161
RN 162
RN 163
RN 164
RN 165
RN 166
RN 167
RN 168
RN 169
RN 170
RN 171
RN 172
RN 173
RN 174
RN 175
RN 176
RN 177
RN 178
RN 179
RN 180
RN 181
RN 182
RN 183
RN 184
RN 185
RN 186
RN 187
RN 188
RN 189
RN 190
RN 191
RN 192
RN 193
RN 194
RN 195
RN 196
RN 197
RN 198
RN 199
RN 200
RN 201
RN 202
RN 203
RN 204
RN 205
RN 206
RN 207
RN 208
RN 209
RN 210
RN 211
RN 212
RN 213
RN 214
RN 215
RN 216
RN 217
RN 218
RN 219
RN 220
RN 221
RN 222
RN 223
RN 224
RN 225
RN 226
RN 227
RN 228
RN 229
RN 230
RN 231
RN 232
RN 233
RN 234
RN 235
RN 236
RN 237
RN 238
RN 239
RN 240
RN 241
RN 242
RN 243
RN 244
RN 245
RN 246
RN 247
RN 248
RN 249
RN 250
RN 251
RN 252
RN 253
RN 254
RN 255
RN 256
RN 257
RN 258
RN 259
RN 260
RN 261
RN 262
RN 263
RN 264
RN 265
RN 266
RN 267
RN 268
RN 269
RN 270
RN 271
RN 272
RN 273
RN 274
RN 275
RN 276
RN 277
RN 278
RN 279
RN 280
RN 281
RN 282
RN 283
RN 284
RN 285
RN 286
RN 287
RN 288
RN 289
RN 290
RN 291
RN 292
RN 293
RN 294
RN 295
RN 296
RN 297
RN 298
RN 299
RN 300
RN 301
RN 302
RN 303
RN 304
RN 305
RN 306
RN 307
RN 308
RN 309
RN 310
RN 311
RN 312
RN 313
RN 314
RN 315
RN 316
RN 317
RN 318
RN 319
RN 320
RN 321
RN 322
RN 323
RN 324
RN 325
RN 326
RN 327
RN 328
RN 329
RN 330
RN 331
RN 332
RN 333
RN 334
RN 335
RN 336
RN 337
RN 338
RN 339
RN 340
RN 341
RN 342
RN 343
RN 344
RN 345
RN 346
RN 347
RN 348
RN 349
RN 350
RN 351
RN 352
RN 353
RN 354
RN 355
RN 356
RN 357
RN 358
RN 359
RN 360
RN 361
RN 362
RN 363
RN 364
RN 365
RN 366
RN 367
RN 368
RN 369
RN 370
RN 371
RN 372
RN 373
RN 374
RN 375
RN 376
RN 377
RN 378
RN 379
RN 380
RN 381
RN 382
RN 383
RN 384
RN 385
RN 386
RN 387
RN 388
RN 389
RN 390
RN 391
RN 392
RN 393
RN 394
RN 395
RN 396
RN 397
RN 398
RN 399
RN 400
RN 401
RN 402
RN 403
RN 404
RN 405
RN 406
RN 407
RN 408
RN 409
RN 410
RN 411
RN 412
RN 413
RN 414
RN 415
RN 416
RN 417
RN 418
RN 419
RN 420
RN 421
RN 422
RN 423
RN 424
RN 425
RN 426
RN 427
RN 428
RN 429
RN 430
RN 431
RN 432
RN 433
RN 434
RN 435
RN 436
RN 437
RN 438
RN 439
RN 440
RN 441
RN 442
RN 443
RN 444
RN 445
RN 446
RN 447
RN 448
RN 449
RN 450
RN 451
RN 452
RN 453
RN 454
RN 455
RN 456
RN 457
RN 458
RN 459
RN 460
RN 461
RN 462
RN 463
RN 464
RN 465
RN 466
RN 467
RN 468
RN 469
RN 470
RN 471
RN 472
RN 473
RN 474
RN 475
RN 476
RN 477
RN 478
RN 479
RN 480
RN 481
RN 482
RN 483
RN 484
RN 485
RN 486
RN 487
RN 488
RN 489
RN 490
RN 491
RN 492
RN 493
RN 494
RN 495
RN 496
RN 497
RN 498
RN 499
RN 500
RN 501
RN 502
RN 503
RN 504
RN 505
RN 506
RN 507
RN 508
RN 509
RN 510
RN 511
RN 512
RN 513
RN 514
RN 515
RN 516
RN 517
RN 518
RN 519
RN 520
RN 521
RN 522
RN 523
RN 524
RN 525
RN 526
RN 527
RN 528
RN 529
RN 530
RN 531
RN 532
RN 533
RN 534
RN 535
RN 536
RN 537
RN 538
RN 539
RN 540
RN 541
RN 542
RN 543
RN 544
RN 545
RN 546
RN 547
RN 548
RN 549
RN 550
RN 551
RN 552
RN 553
RN 554
RN 555
RN 556
RN 557
RN 558
RN 559
RN 560
RN 561
RN 562
RN 563
RN 564
RN 565
RN 566
RN 567
RN 568
RN 569
RN 570
RN 571
RN 572
RN 573
RN 574
RN 575
RN 576
RN 577
RN 5
```

[illegible]

```

Db      69  EEPDETTADDRHKVSTVSLGDNLVQVORWDGKETKFPVREIKGKGMVMTLTFEGVQAVRT 128
QY      131  YEK 133
        |||
Db      129  YEK 131

RESULT 15
Q8UVG7  PRELIMINARY;          PRT;      133  AA.
ID      Q8UVG7
AC      Q8UVG7;
DT      01-MAR-2002 (T-EMBLrel. 20, Created)
DT      01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE      ococyte-type fatty-acid binding protein.
OS      Brachydanio rerio (Zebrafish) (Zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Liu R.-Z., Denovan-Wright E.M., Wright J.M.;
RL      EMBL; AF448057; AAL40832.1; -
DR      Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR      InterPro; IPR000463; Fatty_acid_BP.
DR      InterPro; IPR000566; Lipocln_cytFABP.
DR      Pfam; PF00061; lipocalin; 1.
DR      PRINTS; PR00178; FATTYACIDBP.
DR      PROSITE; PS00214; FABP; UNKNOWN_1.
SQ      SEQUENCE 133 AA; 14882 MW; 91FB0400619A1926 CRC64;

Query Match          41.9%; Score 299; DB 13; Length 133;
Best Local Similarity 45.7%; Pred. No. 14e-22;
Matches 58; Conservative 24; Mismatches 45; Indels 0; Gaps

QY      9  GKWRMLMSGHFEYMKELGYGLALRKMAAMAKPDCITCDGNNTVKTSTVKTTFVSCN 68
Db      7  GTWNLKSKNPFDEYMKIGVGFATQVANNMKTPTTIISKEGDVFTLKTVSTFKSTEINFK 66

QY      69  LGKEFDETTADGRKTEVTCFQDQALVQHOQWQKGSTETTRKLKDGKIMVECVNNATCT 128
        |||:||||||| ||: ||: |:||||: ||: |:||: ||: ||: ||: ||: |
Db      67  LGEEFDETTADRRKVKSVITLDGGKLLHVQKWQDGKETTLRLREVSDDNLLTLTLGLDIVST 126
        |||:||||||| ||: ||: |:||||: ||: |:||: ||: ||: ||: ||: |

QY      129  RVYEVQV 135
        |||:
Db      127  RHYVKA 133

Search completed: November 25, 2002, 10:24:43
Job time : 33 secs

```

Search completed: November 25, 2002, 10:24:43
Job time : 33 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:19:57 ; Search time 12 Seconds
(without alignments)
466.609 Million cell updates/sec

Title: US-09-788-074-1
Perfect score: 713
Sequence: 1 MASLKDLGKRLMESHGFE.....MIVECMNNAATCTRVYKVKQ 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	713	100.0	135	1 FABE_MOUSE	Q05816 mus musculus
2	663	93.0	135	1 FABE_RAT	P55053 rattus norv
3	612	85.8	135	1 FABE_HUMAN	Q01469 homo sapien
4	577	80.9	135	1 FABE_BOVIN	P55052 bos taurus
5	391	54.8	131	1 MYP2_RABIT	P02691 oryctolagus
6	380	53.3	131	1 MYP2_HUMAN	P02689 homo sapien
7	375	52.6	131	1 FABA_BOVIN	P48035 bos taurus
8	373	52.3	131	1 FABA_PIG	Q97788 sus scrofa
9	370	51.9	131	1 FABA_SPETR	Q9960 spermophilu
10	369	51.8	131	1 MYP2_MOUSE	P24526 mus musculus
11	367	51.5	131	1 MYP2_BOVIN	P02690 bos taurus
12	364	51.1	132	1 FABL_GINGCI	P80049 ginglymosto
13	362	50.8	131	1 FABA_HUMAN	P15090 homo sapien
14	359	50.4	131	1 FABA_MOUSE	P04117 mus musculus
15	336	47.1	132	1 FABA_RAT	P07483 rattus norv
16	335	47.0	131	1 FABA_RAT	P70623 rattus norv
17	334	46.8	132	1 FABH_SPETR	Q99661 spermophilu
18	333	46.7	132	1 FABH_HUMAN	P05413 homo sapien
19	331	46.4	132	1 FABH_PIG	Q02772 sus scrofa
20	320	44.9	132	1 FABH_BOVIN	P10790 bos taurus
21	320	44.9	132	1 TLBP_MOUSE	Q08716 mus musculus
22	320	44.9	132	1 TLBP_RAT	P55054 rattus norv
23	318	44.6	132	1 FABH_MOUSE	P11404 mus musculus
24	308	43.2	131	1 FABB_CHICK	Q05423 gallus gall
25	302	42.4	131	1 FABB_BOVIN	Q09139 bos taurus
26	292	41.0	131	1 FABB_HUMAN	O15540 homo sapien
27	290	40.7	132	1 FABB_ONCMY	O13088 oncorhynch
28	282	39.6	131	1 FABB_MOUSE	P13800 mus musculus
29	281	39.4	131	1 FABB_RAT	P55051 rattus norv
30	273	38.3	114	1 FABL_LAMJA	P82188 lampetra ja
31	215.5	30.2	137	1 RET3_HUMAN	P50568 xenopus lae
32	213.5	29.9	133	1 FABP_ECHGR	Q02970 echinococcu
33	213.5	29.9	137	1 RET4_HUMAN	P29373 homo sapien

ALIGNMENTS

RESULT 1

ID	FABE_MOUSE	STANDARD;	PRT;	135 AA.
AC	Q05816;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Patty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (FA-FABP) (Keratinocyte lipid-binding protein).			
DE	fatty acid-binding protein homolog (FA-FABP) (Keratinocyte lipid-binding protein).			
GN	FABP5 OR MALL OR KLBP OR FABPE.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Keratinocytes;			
RX	MEDLINE=93352523; PubMed=8349619;			
RA	Krieg P., Feil S., Fuerstenberger G., Bowden T.G.;			
RT	"Tumor-specific overexpression of a novel keratinocyte lipid-binding protein. Identification and characterization of a cloned sequence activated during multistage carcinogenesis in mouse skin.";			
RL	J. Biol. Chem. 268:17362-17369(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ;			
RX	MEDLINE=98332726; PubMed=9666100;			
RA	Bleck B., Hohoff C., Binas B., Rustow B., Dixkens C., Hamelster H., Boerchers T., Spener F.;			
RT	"Cloning and chromosomal localisation of the murine epidermal-type fatty acid binding protein gene (Fabpe).";			
RL	Gene 215:123-130(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99013878; PubMed=9795232;			
RA	Hertzel A.V., Bernlohr D.A.;			
RT	"Cloning and chromosomal location of the murine Keratinocyte lipid-binding protein gene.";			
RL	Gene 221:235-243(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Stomach;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			

34	212	29.7	136	1 RET3_HUMAN	P29762 homo sapien
35	209.5	29.4	137	1 RET4_MOUSE	P22935 mus musculus
36	209	29.3	136	1 RET3_MOUSE	P02695 mus musculus
37	208	29.2	136	1 RET3_FUGRU	O42386 fugu rubrip
38	197.5	27.7	133	1 FABP_SCHMA	P29498 schistosoma
39	195	27.3	138	1 RET4_RAT	P51673 rattus norv
40	189	26.5	130	1 FABP_BLOTA	Q17284 blomia trop
41	187	26.2	120	1 RET3_CHICK	P40220 gallus gall
42	187	26.2	134	1 RET1_RAT	P02696 rattus norv
43	186	26.1	134	1 RET1_HUMAN	P09455 homo sapien
44	183	25.7	134	1 RET5_HUMAN	P82980 homo sapien
45	181	25.4	133	1 FABM_LOEMI	P41509 locusta mig

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA Hayashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX Strausberg R.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN KERATINOCYTES AND ALSO IN
CC STRATIFIED EPITHELIA OF EPIDERMIS AND TONGUE. RELATIVELY HIGH
CC LEVELS FOUND IN ADIPOSE AND MAMMARY TISSUES AND SMALL AMOUNTS
CC FOUND IN HEART, BRAIN, LIVER, SPLEEN, MUSCLE AND LUNG.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70100; CA449703.1; -;
DR EMBL; AJ223066; CA411069.1; -;
DR EMBL; AF061015; AAC82368.1; -;
DR EMBL; AF061014; AAC82368.1; JOINED.
DR EMBL; AK008782; BAB25890.1; -;
DR EMBL; AK011551; BAB27692.1; -;
DR EMBL; BC002008; AAH02008.1; -;
DR PIR; S36635; S36635.
DR HSSP; Q01469; 1B56.
DR MGD; MGI:101790; Fabbp5.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPP; 1.
KW Transport; Lipid-binding.
SQ SEQUENCE 135 AA; 15137 MW; 6A6C8DBEB046185 CRC64;

Query Match 100.0%; Score 713; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 2e-64;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTV 60
DB 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTV 60

QY 61 KTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQWQDGKSTITRKLKDGKMWEC 120
DB 61 KTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQWQDGKSTITRKLKDGKMWEC 120

QY 121 VMNNATCTRYEKVQ 135
DB 121 VMNNATCTRYEKVQ 135

RESULT 2
FABE_RAT STANDARD; PRT; 135 AA.
AC P5053; p97757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Fatty acid-binding protein, epidermal (E-FABP) (Cutaneous fatty acid-
DE binding protein) (c-FABP) (DALI).
GN FABP5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lens;
RX MEDLINE=95331629; PubMed=7607553;
RA Wen Y., Li G.W., Chen P., Wong E., Bekhor I.;
RT "Lens epithelial cell mRNA, II. Expression of a mRNA encoding a
RT lipid-binding protein in rat lens epithelial cells.";
RL Gene 158:269-274(1995).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RX MEDLINE=94220094; PubMed=8166694;
RA Watanabe R., Fujii H., Odani S., Sakakibara J., Yamamoto A., Ito M.,
RA Ono T.;
RT "Molecular cloning of a cDNA encoding a novel fatty acid-binding
RT protein from rat skin.";
RL Biochem. Biophys. Res. Commun. 200:253-259(1994).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Nerve;
RX MEDLINE=96302634; PubMed=8723767;
RA De Leon M., Welcher A.A., Nahin R.H., Liu Y., Ruda M.A.,
RA Shooter E.M., Molina C.A.;
RT "Fatty acid binding protein is induced in neurons of the dorsal root
RT ganglia after peripheral nerve injury.";
RL J. Neurosci. Res. 44:283-292(1996).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U13253; AAA86680.1; -;
DR EMBL; S69874; AAB30574.1; -;
DR EMBL; S83247; AAB46848.1; -;
DR HSSP; Q01469; 1B56.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPP; 1.
KW Transport; Lipid-binding.
FT CONFLICT 49 49 G -> N (IN REF. 1).
FT CONFLICT 112 112 K -> N (IN REF. 3).
SQ SEQUENCE 135 AA; 15059 MW; 978392433DF54358 CRC64;

Query Match 93.0%; Score 663; DB 1; Length 135;
Best Local Similarity 91.9%; Pred. No. 1.9e-59;
Matches 124; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAMAKPDCIITCDGNITVKTSTV 60
DB 1 MASLKDEGKRWLMESHGFEYMKELGVGLALRKMAAMAKPDCIITLDGNNITVKTSTV 60

QY 61 KTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQWQDGKSTITRKLKDGKMWEC 120
DB 61 KTVFSCNLGKGFDETTADGRKTETVCTFDGALVQHQWQDGKSTITRKLKDGKMWEC 120

QY 121 VMNNATCTRYEYKQ 135
Db 121 VMNNAICTRYEYKQ 135

RESULT 3
FABE_HUMAN
ID FABE_HUMAN STANDARD; PRT; 135 AA.
AC Q01469;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
DE fatty acid-binding protein homolog) (PA-FABP).
GN FABP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Keratinocytes;
RX MEDLINE=92381332; PubMed=1512466;
RA Madsen P.S., Rasmussen H.H., Jeffers H., Honore B., Celis J.E.;
RT "Molecular cloning and expression of a novel keratinocyte protein
RT (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is
RT highly up-regulated in psoriatic skin and that shares similarity to
RT fatty acid-binding proteins.";
RL J. Invest. Dermatol. 99:299-305(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [4]
RP SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
RX MEDLINE=94379963; PubMed=8092987;
RA Siegenthaler G., Hotz R., Chatellard-Gruaz D., Didierjean L.,
RA Hellman U., Saurat J.-H.;
RT "Purification and characterization of the human epidermal fatty acid-
RT binding protein: localization during epidermal cell differentiation
RT in vivo and in vitro.";
RL Biochem. J. 302:363-371(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=99425110; PubMed=10493790;
RA Hohoff C., Borchers T., Rustow B., Spener F., van Tilbeurgh H.;
RT "Expression, purification and crystal structure determination of
RT recombinant human epidermal-type fatty acid-binding protein.";
RL Biochemistry 38:12229-12239(1999).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH. DECREASING THE CHAIN LENGTH OR INTRODUCING
CC DOUBLE BONDS REDUCES THE AFFINITY. MAY BE INVOLVED IN KERATINOCYTE
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: KERATINOCYTES; HIGHLY EXPRESSED IN PSORIATIC
CC SKIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M94856; AAA58467.1; -;
DR EMBL; BC019385; AAH19385.1; -;
DR PDB; 1B56; 05-OCT-99.
DR Aarhus/Ghent-2DPAGE; 3007; IEF.
DR Genew; HGNC:3560; FABP5.
DR MIM; 605168; -;
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; 3D-structure.
SQ SEQUENCE 135 AA; 15164 MW; 77D38F8806143D63 CRC64;
Query Match 85.8%; Score 612; DB 1; Length 135;
Best Local Similarity 80.0%; Pred. No. 2.4e-54;
Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
QY 1 MASLKDECKWRIMESHGFEYMKELGVGLALPKMAAMAKPDCIITCDGNITVKTESTV 60
Db 1 MATVQQLGKRWRLVDSKGFDEYNKELGVGLALPKMAAMAKPDCIITCDGNLTKTESTL 60
QY 61 KTVFSCNLGERKFDETADGRKTETCTFQDGALVQHQQWQDGKKESTITRKLKDKRMIVEC 120
Db 61 KITQFSCTLGKFEETADGRKTQTVCNFTDGLVQHQQWQDGKKESTITRKLKDKLVVEC 120
QY 121 VMNNATCTRYEYKQ 135
Db 121 VMNVTCTRIYEKVE 135

RESULT 4
FABE_BOVIN
ID FABE_BOVIN STANDARD; PRT; 135 AA.
AC P55052; O62808;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Differentiation-
DE associated lipid binding protein LP2).
GN FABP5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-33 AND 116-129.
RC TISSUE=Lens;
RX MEDLINE=97103094; PubMed=8947466;
RA Jaworski C., Wistow G.;
RT "LP2, a differentiation-associated lipid-binding protein expressed in
RT bovine lens.";
RL Biochem. J. 320:49-54(1996).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=98198033; PubMed=9521644;
RA Kingma P.B., Bok D., Ong D.E.;
RT "Bovine epidermal fatty acid-binding protein: determination of ligand
RT specificity and cellular localization in retina and testis.";
RL Biochemistry 37:3250-3257(1998).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC THE UNSATURATED FATTY ACID PALMITATE (C16:0). MAY BE INVOLVED IN
CC THE UPTAKE AND TRANSPORT OF FATTY ACIDS ESSENTIAL FOR THE
CC NOURISHMENT OF THE SURROUNDING CELL TYPES. IT IS A POTENTIAL
CC TARGET FOR OXIDATIVE STRESS DURING CATARACT FORMATION IN LENS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LENS AND RETINA (FOUND IN THE

```

CC MUeller cells), MODERATELY ABUNDANT IN HEART AND TESTIS (FOUND IN
CC THE SEROTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U55188; AAC14297.1; -.
CC EMBL; AF059507; AAC14711.1; -.
CC HSP; O01469; 1B56.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam: PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding; Phosphorylation.
CC MOD_RES 22 22 PHOSPHORYLATION (BY TYR-KINASES)
CC FT CONFLICT 52 52 L -> P (IN REF. 1).
CC FT CONFLICT 135 AA; 15074 MW; 439886AF88A34E2A CRG64;
CC SEQUENCE 135 AA; 15074 MW; 439886AF88A34E2A CRG64;
CC -----
Query Match 80.9%; Score 577; DB 1; Length 135;
Best Local Similarity 76.3%; Pred. No. 7.6e-51;
Matches 103; Conservative 20; Mismatches 12; Indels 0; Gaps 0;
CC QY 1 MASLKDEGKRWLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTV 60
CC Db 1 MATVQOLVGRWRLVESGFDEYKVGCVGNALRKVGAMAKPDCIITSDGKNLSIKTESTL 60
CC QY 61 KTVFSCNLGEKEDETTADGRKTETVCTFODGALVQHQWDGKESTITRKLKDKGMIVEC 120
CC Db 61 KTFQFCKLGEKEETADGRKTQTCNFTDGLVQHQWDGKESTITRKLKDKGLVVVC 120
CC QY 121 VMNNAVCTRYVEKVO 135
CC Db 121 VMNNAVCTRYVEKVE 135
CC -----
RESULT 5
MYP2_RABIT STANDARD; PRT; 131 AA.
AC P02691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228063; PubMed=2453513;
RA Narayanan V., Barbosa E., Reed R., Tennekoon G.;
RT "Characterization of a cloned cDNA encoding rabbit myelin P2
RT protein.";
RL J. Biol. Chem. 263:8332-8337(1988).
RN [2]
RP SEQUENCE OF 1-55.
RX MEDLINE=80094496; PubMed=7356651;
RA Ishaque A., Hofmann T., Rhee S., Eylar E.H.;
RT "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT myelin.";
RL J. Biol. Chem. 255:1058-1063(1980).
RN [3]
RP SEQUENCE OF 55-131.

```

```

RX MEDLINE=82098098; PubMed=6172423;
RA Ishaque A., Hofmann T., Eylar E.H.;
RT "The complete amino acid sequence of the rabbit P2 protein.";
RL J. Biol. Chem. 257:592-595(1982).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03744; AAA31451.1; -.
CC PIR; A03145; MPRB2.
CC PIR; A28081; A28081.
CC HSP; P02690; IPMP.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam: PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Myelin; Lipid-binding; Transport; Acetylation.
CC INIT_MET 0 0
CC MOD_RES 1 1 ACETYLATION.
CC CONFLICT 72 72 E -> Q (IN REF. 3).
CC CONFLICT 83 83 I -> T (IN REF. 3).
CC CONFLICT 98 98 D -> N (IN REF. 3).
CC SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRG64;
CC -----
Query Match 54.8%; Score 391; DB 1; Length 131;
Best Local Similarity 57.9%; Pred. No. 2.8e-32;
Matches 73; Conservative 22; Mismatches 31; Indels 0; Gaps 0;
CC QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVTKTVFSCN 68
CC Db 6 GTMKLVSSFNDDYMKALGVGLATRLKGLAKPNVIISKKGDIITRTTESTFKNTSEISPK 65
CC QY 69 LGEKFDETTADGRKTETVCTFODGALVQHQWDGKESTITRKLKDKGMIVECVNNATCT 128
CC Db 66 LGQEFEEETADNRKTSIITLGERGALNQVQKDGKETTITRKLKLVGKVMVVECKMGVVC 125
CC QY 129 RYVEKV 134
CC Db 126 RYVEKV 131
CC -----
RESULT 6
MYP2_HUMAN STANDARD; PRT; 131 AA.
AC P02689;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92068191; PubMed=1720307;
RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;
RT "Isolation and sequence determination of cDNA encoding P2 protein of
RT

```

```

RT human peripheral myelin.";
RL Biochem. Biophys. Res. Commun. 181:204-207(1991).
RN [2]
RP SEQUENCE.
RX MEDLINE=83058785; PubMed=6183401;
RA Suzuki M., Kitamura K., Sakamoto Y., Uyenura K.;
RL "The complete amino acid sequence of human P2 protein.";
RT J. Neurochem. 39:1759-1762(1982).
RN [3]
RP SEQUENCE OF 1-115 FROM N.A.
RX MEDLINE=95054012; PubMed=7525873;
RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
RA Tennekoon G.;
RL "Partial structure and mapping of the human myelin P2 protein gene.";
RT J. Neurochem. 63:2010-2013(1994).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D16181; BAA03726.1; -.
DR EMBL; D16179; BAA03726.1; JOINED.
DR EMBL; D16180; BAA03726.1; JOINED.
DR EMBL; X62167; CAA44096.1; -.
DR EMBL; S73470; AAB32592.2; -.
DR EMBL; S73468; AAB32592.2; JOINED.
DR EMBL; S73469; AAB32592.2; JOINED.
DR PIR; A03143; MPH02.
DR PIR; JTO977; JTO977.
DR HSSP; P02690; LPWP.
DR Genew; HGNC:9117; PMP2.
DR MIM; 170715; -.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLTATION.
FT DISULFID 117 124
FT CONFLICT 24 24 G -> GG (IN REF. 3).
FT CONFLICT 98 98 D -> N (IN REF. 2).
FT CONFLICT 110 110 N -> D (IN REF. 2).
SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;

Query Match 53.3%; Score 380; DB 1; Length 131;
Best Local Similarity 56.3%; Pred. No. 3.5e-31;
Matches 71; Conservative 22; Mismatches 33; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKALGVGLATRLGNLAKPTVIISKGGDIITRTSTFKNTSEIFK 65

QY 69 LGEKFDFTADGRKTTVTCTFDQGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGOEFEFTADNRKTSIVTLQGRSLNQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 125

QY 129 RYVEKV 134
Db 126 RYVEKV 131

```

```

RESULT 7
FABA_BOVIN STANDARD; PRT; 131 AA.
ID FABA_BOVIN
AC P48035;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
GN FABP4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96355299; PubMed=8702709;
RA Specht B., Bartetzko N., Hohoff C., Kuhl H., Franke R.,
RA Boerchers T., Spener F.;
RT "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RL J. Biol. Chem. 271:19943-19949(1996).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89244; CAA61532.1; -.
DR HSSP; P04117; LLID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 19 19 PHOSPHORYLTATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;

Query Match 52.6%; Score 375; DB 1; Length 131;
Best Local Similarity 55.2%; Pred. No. 1.1e-30;
Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLRLMESHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKELGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 65

QY 69 LGEKFDFTADGRKTTVTCTFDQGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGOEFEFTADNRKTSIVTLQGRSLNQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 125

QY 129 RYVEKV 133
Db 126 RYVEKV 130

```

```

RESULT 8
FABA_PIG STANDARD; PRT; 131 AA.
ID FABA_PIG
AC O97788;

```

```
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (AP2).
GN FABP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Duroc; TISSUE=Liver;
RX MEDLINE=99099248; PubMed=9880671;
RA Gerbens F.N.A., Jansen A., van Erp A.J.M., Harders F.,
RA Meuwissen T.H.E., Rettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;
RT "The adipocyte fatty acid-binding protein locus: characterization and
RT association with intramuscular fat content in pigs.";
RL Mamm. Genome 9:1022-1026(1998).
RN [2]
RP SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.
RC TISSUE=Fat;
RX MEDLINE=90241143; PubMed=2334399;
RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
RT "The purification and characterization of a fatty acid binding protein
RT specific to pig (Sus domesticus) adipose tissue.";
RL Biochem. J. 267:373-378(1990).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF INTRAMUSCULAR FAT
CC ACCRETION.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: ADIPOSE TISSUE.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/FAMILY OF
CC TRANSPORTERS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y16039; CAA75995.1; -.
DR EMBL; AJ416020; CAC95166.1; -.
DR HSSP; P04117; 1L1D.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000366; Lipocin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
FT SEQUENCE 131 AA; 14545 MW; 656CB0CA08CDA82 CRC64;
Query Match 52.3%; Score 373; DB 1; Length 131;
Best Local Similarity 53.6%; Pred. No. 1.8e-30;
Matches 67; Conservative 25; Mismatches 33; Indels 0; Gaps 0;
QY 9 GKWRLMESHGFEEYMKELGVGLALRRKMAAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
DB 6 GTWKLVSSENFDDYMKVEGVGFATRKVAGMARNLIITVNGDMITIRSESTFKNTETIAFK 65
QY 69 LGKEFDETTADGKRTVCTVCTFDGALVQHQDQKGKSTITRKLKDGKMTIVECVMMNATCT 128
DB 66 LGQEFDEVATDRKVKSTITLDGGALVQVQKQKGTITINRKRVDKLVVEICIMKGVTTAT 125
QY 129 RYVEK 133
DB 126 RYER 130
RESULT 10
MYP2_MOUSE
ID MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
```

```
DB 126 RYER 130
RESULT 9
FABA_SPEPR
ID FABA_SPEPR STANDARD; PRT; 131 AA.
AC Q99P60;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP).
GN FABP4.
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Hittel D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding
RT proteins in hibernating ground squirrels.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/FAMILY OF
CC TRANSPORTERS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF327855; AAK08084.1; -.
DR HSSP; P04117; 1L1D.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000366; Lipocin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
FT SEQUENCE 131 AA; 14634 MW; FCEE7B092A2AF708 CRC64;
Query Match 51.9%; Score 370; DB 1; Length 131;
Best Local Similarity 54.4%; Pred. No. 3.5e-30;
Matches 68; Conservative 24; Mismatches 33; Indels 0; Gaps 0;
QY 9 GKWRLMESHGFEEYMKELGVGLALRRKMAAKPDCIITCDGNNTVKTSTVKTTFVSCN 68
DB 6 GTWKLVSSENFDDYMKVEGVGFATRKVAGMARNLIITVNGDMITIRSESTFKNTETIAFK 65
QY 69 LGKEFDETTADGKRTVCTVCTFDGALVQHQDQKGKSTITRKLKDGKMTIVECVMMNATCT 128
DB 66 LGQEFDEVATDRKVKSTITLDGGALVQVQKQKGTITIKRKRDDKLVVEICIMKGVTTST 125
QY 129 RYVEK 133
DB 126 RYER 130
RESULT 10
MYP2_MOUSE
ID MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
```

```
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S39508; AAB19249.2; -
DR PIR; JH0407; JH0407.
DR HSP; P02690; LPMP.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Query Match 51.8%; Score 369; DB 1; Length 131;
Best Local Similarity 54.0%; Pred. No. 4.5e-30;
Matches 68; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVFSN 68
DB 6 GTWKLVSSEHFDYMKALGVGLANRKLGNLAKPTVIISKGDYITRTESAFKNTSEIFK 65
QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKESTITRKLKDGKMLVECVMNATCT 128
DB 66 LQGEFEETADNRKAKSIVTLERGLSKQVQKWDGKETAIRRTLLDGRMVVECMKGVVCT 125
QY 129 RYVEKV 134
DB 126 RYVEKV 131

RESULT 11
MYP2_BOVIN
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S39508; AAB19249.2; -
DR PIR; JH0407; JH0407.
DR HSP; P02690; LPMP.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Query Match 51.8%; Score 369; DB 1; Length 131;
Best Local Similarity 54.0%; Pred. No. 4.5e-30;
Matches 68; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVFSN 68
DB 6 GTWKLVSSEHFDYMKALGVGLANRKLGNLAKPTVIISKGDYITRTESAFKNTSEIFK 65
QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKESTITRKLKDGKMLVECVMNATCT 128
DB 66 LQGEFEETADNRKAKSIVTLERGLSKQVQKWDGKETAIRRTLLDGRMVVECMKGVVCT 125
QY 129 RYVEKV 134
DB 126 RYVEKV 131

RESULT 11
MYP2_BOVIN
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
```

```
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80225120; PubMed=6156092;
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;
RT "The complete amino acid sequence of the P2 protein in bovine
RT peripheral nerve myelin.";
RL FEBS Lett. 115:27-30(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=89005045; PubMed=2458918;
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;
RT "The three-dimensional structure of P2 myelin protein.";
RL EMBO J. 7:1597-1604(1988).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=93253782; PubMed=7683727;
RA Cowan S.W., Newcomer M.E., Jones T.A.;
RT "Crystallographic studies on a family of cellular lipophilic
RT transport proteins. Refinement of P2 myelin protein and the structure
RT determination and refinement of cellular retinol-binding protein in
RT complex with all-trans-retinol.";
RL J. Mol. Biol. 230:1225-1246(1993).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC PIR; A03144; MPB02.
CC PDB; 1PMP; 26-JAN-95.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocalin_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
FT MOD_RES 1 1 ACETYLATION.
FT DISULFD 117 124
SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Query Match 51.5%; Score 367; DB 1; Length 131;
Best Local Similarity 55.6%; Pred. No. 7.1e-30;
Matches 70; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 9 GKWLMEHGFEEYMKELGVGLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVFSN 68
DB 6 GTWKLVSSEHFDYMKALGVGLANRKLGNLAKPTVIISKGDYITRTESAFKNTSEIFK 65
QY 69 LGEKFEDETTADGRKKTETVCTFODGALVQHQWDGKESTITRKLKDGKMLVECVMNATCT 128
DB 66 LQGEFEETADNRKKTSTVTLARGSLNQVQKWNGETTITRKLVDGKMWVECKMKDVVCT 125
QY 129 RYVEKV 134
DB 126 RYVEKV 131

RESULT 12
FABL_GINCI
ID FABL_GINCI STANDARD; PRT; 132 AA.
AC P80049;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Fatty acid-binding protein, liver (L-FABP).
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Ginglymostomatidae; Ginglymostoma.
OX NCBI_TaxID=7801;
```


Zhang J., Rickers-Haunlerland J., Dave I., Haunerland N.H.;
"Structure and chromosomal location of the rat gene encoding the heart
fatty acid-binding protein.";
Eur. J. Biochem. 266:347-351(1999).
[7]
SEQUENCE OF 58-86.
MEDLINE=69374061; PubMed=2775193;
Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
"Rat heart fatty acid-binding protein. Evidence that supports the
amino acid sequence predicted from the cDNA.";
Biochem. J. 260:303-306(1989).
[8]
PARTIAL SEQUENCE.
TISSUE=Stomach;
MEDLINE=90032682; PubMed=2806260;
Kanda T., Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,
Matsubara Y., Muto T., Ono T.;
"Purification and characterization of a fatty-acid-binding protein
from the gastric mucosa of rats. Possible identity with heart
fatty-acid-binding protein and its parietal cell localization.";
Eur. J. Biochem. 185:27-33(1989).
[9]
PARTIAL SEQUENCE.
TISSUE=Mammary gland;
MEDLINE=94162301; PubMed=8117746;
Nielsen S.U., Rump R., Hoejrup P., Roepstorff P., Spener F.;
"Differentiation regulation and phosphorylation of the fatty acid-
binding protein from rat mammary epithelial cells.";
Biochim. Biophys. Acta 1211:189-197(1994).
-!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,
BRAIN AND MAMMARY GLAND.
-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
TRANSPORTERS.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; J02773; AAA41136.1; -
EMBL; M18034; AAA41137.1; -
EMBL; AF144090; AAF19003.1; -
PIR; A23838; A23838.
PIR; A27452; A27452.
PIR; A28197; A28197.
PIR; A28458; A28458.
PIR; A39551; A39551.
PIR; S06478; S06478.
HSP; P05413; LHMT
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; Lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Acetylation; Phosphorylation.
FT INIT_MET 0 0
MOD_RES 1 1 ACETYLATION.
MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES).
CONFLICT 63 63 S -> SN (IN REF. 3).
FT

```

FT CONFLICT 69 69 E -> Q (IN REF. 5).
FT CONFLICT 70 70 F -> D (IN REF. 3).
FT CONFLICT 115 115 L -> LL (IN REF. 6).
SQ SEQUENCE 132 AA; 14643 MW; 31B4C6GA8BFB45BE CRC64;

Query Match 47.1%; Score 336; DB 1; Length 132;
Best Local Similarity 51.2%; Pred. No. 8.9e-27;
Matches 64; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 9 GKWRLMESHGFEYMKELGVLALRKMAAMAKPDCIITCDGNNITVKTESTVKTTFVSCN 68
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
Db 6 GTWKLVDSKNFDDYMKSLGSGVGFATROVASMTKPTTIIERNKGDITTIKTHSTPKNTEISFQ 65
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
QY 69 LGEKFDETTADGRKTTVCTFQDQALVQHQQWDGKESTITRKLKDGKMIVECVMMNATCT 128
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
Db 66 LGVFDEVTADDRKVKSVVTLDDGKLVHVQKWDGQETTLTRELSDGKLLTLTHGNVST 125
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
QY 129 RVYEK 133
   |:::|
Db 126 RYEK 130
   .

Search completed: November 25, 2002, 10:24:05
Job time : 13 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:34:08 ; Search time 30 Seconds

(without alignments)
927.212 Million cell updates/sec

Title: US-09-788-074-3

Perfect score: 711

Sequence: 1 MATVQQLBGRRLVDSKGF.....LVVECMNVNVTCTRIYKVE 135

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mmc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertibrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374	52.6	132	13 Q90X55	Q90X55 gallus gall
2	369	51.9	132	11 Q9DAK4	Q9DAK4 mus musculus
3	359	50.5	132	13 Q8QHA8	Q8QHA8 anser anser
4	334	47.0	150	11 Q9R290	Q9R290 rattus norv
5	333	46.8	132	13 Q90W92	Q90W92 fundulus he
6	331.5	46.6	134	13 Q57665	Q57665 gobionototh
7	331.5	46.6	134	13 Q57691	Q57691 cryodraco a
8	330	46.4	132	11 Q9DAL2	Q9DAL2 mus musculus
9	329.5	46.3	134	13 Q57666	Q57666 paraheanic
10	329	46.3	113	6 Q9XSG4	Q9XSG4 oryctolagus
11	327.5	46.1	134	13 Q57663	Q57663 notothenia
12	326	45.9	135	13 Q91896	Q91896 anguilla ja
13	320	45.0	125	6 Q9XS15	Q9XS15 equus cabal
14	313	44.0	132	13 Q918N9	Q918N9 brachydanio
15	304	42.8	133	13 Q8UVG7	Q8UVG7 brachydanio
16	296	41.6	133	13 Q57668	Q57668 cryodraco a

17	295	41.5	133	13	Q57667	O57667.chaenocepha
18	295	41.5	133	13	Q57670	O57670.gobionototh
19	295	41.5	136	5	Q8WR15	Q8WR15.metapanaeus
20	294	41.4	133	13	Q57669	O57669.notothenia
21	281	39.5	166	4	Q9H047	Q9H047.homo.sapien
22	277	39.0	99	6	O97675	O97675.sus.scrofa
23	256	36.0	111	13	Q90ZG6	Q90ZG6.brachydanio
24	253.5	35.7	130	5	O9VGM2	O9VGM2.drosophila
25	253	35.6	152	5	Q965W1	Q965W1.caenorhabdi
26	244.5	34.4	100	13	Q57664	O57664.rhigophila
27	234.5	33.0	135	5	O01812	O01812.caenorhabdi
28	231.5	32.6	137	5	O02323	O02323.caenorhabdi
29	230	32.3	86	13	Q8UWD3	Q8UWD3.anser.anser
30	224.5	31.6	136	5	O01814	O01814.caenorhabdi
31	222.5	31.3	133	5	Q9BMK1	Q9BMK1.echinococcu
32	222.5	31.3	133	5	Q9BLY5	Q9BLY5.echinococcu
33	222	31.2	97	11	Q9QV90	Q9QV90.mus.sp.lmg
34	215.5	30.3	133	5	O967X3	O967X3.echinococcu
35	211.5	29.7	132	5	O61236	O61236.manduca.sex
36	209.5	29.5	132	5	Q9UIG6	Q9UIG6.fasciola.he
37	209.5	29.5	133	5	Q9BMK2	Q9BMK2.echinococcu
38	208.5	29.3	133	5	Q9BMK3	Q9BMK3.echinococcu
39	200.5	28.2	132	5	O26517	O26517.schistosoma
40	194.5	27.4	147	13	Q9PSA5	Q9PSA5.xenopus.lae
41	192.5	27.1	132	5	Q9BWE8	Q9BWE8.schistosoma
42	191.5	26.9	132	5	O45035	O45035.schistosoma
43	184.5	25.9	133	5	Q8T5U9	Q8T5U9.schistosoma
44	171	24.1	128	13	Q919A9	Q919A9.lygodactylu
45	169	23.8	98	5	Q8T5U8	Q8T5U8.schistosoma

ALIGNMENTS

RESULT 1

Q90X55 PRELIMINARY; PRT; 132 AA.

ID Q90X55; Q90X56;

DC Q90X55; Q90X56; (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Adipocyte fatty acid binding protein.

GN AFABP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RA Wang Q., Ao J., Meng H., Zhao J., Li J., Wang Y., Li H.;

RT "Study on chicken AFABP gene as candidate gene for fatness trait.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RA Wang Q., Li N., Li H.;

RT "Cloning and sequencing of adipocyte fatty acid binding protein gene

in chicken.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=FAT;

RA Wang Q., Li N., Li H.;

RT "Cloning and sequencing of adipocyte fatty acid binding protein gene

in chicken.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF432507; AAL30744.2; -

DR EMBL; AF432506; AAL30743.1; -

DR InterPro; IPR000463; Fatty_acid_BP.

DR InterPro; IPR000566; Lipocalin_cytFABP.

DR Pfam; PF00061; lipocalin; 1.

DR PROSITE; PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 132 AA; 14894 MW; 4F5905FAB8DA268B CRC64;

Query Match 52.6%; Score 374; DB 13; Length 132;
Best Local Similarity 54.7%; Pred. No. 1e-30;
Matches 70; Conservative 22; Mismatches 36; Indels 0; Gaps 0;

QY 6 QLEGWRVLDSKGFDEYMKELVGIALRKGAMAKPCDIITCDGNLTIKTSTLTQTQF 65
Db | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
4 QFVGTWLLSSENFEDYMKELVGVGFATRKMGAGVKPNLTISINGDVITIRSESTFKNTEI 63

QY 66 SCTLGEXFEETADGRKTOTVCNTFDGALVOHQEWDKGESTITRKLKDGLKVCEVMNV 125
Db | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
64 SFKLGESEFDETADRRTKNVTILDSGLTKQVKWDGKETVIKRKYVDGNLLVECTMNV 123

QY 126 TCTRIVK 133
Db | |:| :|:

QY 124 TSKRVYER 131
Db | |:| :

RESULT 2
Q9DAKA PRELIMITARY; PRT; 132 AA.

ID Q9DAK4 AC QPAKA;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE L700008G05RIk protein.
GN L700008G05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musineae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingagawa A., Shibata K., Yonohino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirali L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Anjo H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Humé D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momabaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasakui H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa H., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RM ENBL; AK005765; BAB24227.1; - .
DR HSSP; P02690; 1PMF
DR MGDR; MGI:1922747; L700008G05RIK.
DR InterPro; IPRO000463; Fatty_acid_BP.
DR InterPro; IPRO00566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTVACIDBP.
SQ SEQUENCE 132 AA; 14758 MW; 7A20C53780845F61 CRC64;

Query Match 51.9%; Score 369; DB 11; Length 132;
Best Local Similarity 54.2%; Pred. No. 3.4e-30;
Matches 71; Conservative 22; Mismatches 38; Indels 0; Gaps 0;

QY 4 VOQLGWRLVDSKGFDEYMKELVGIALRKMGMAPDCDIITCDGNLTIKTSTLTQT 63
Db | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
2 VDOLQGFWKSVCDFNFENYMKELVGSRSLKGLCAKPTTISTPDGLIITIKTSIFKNK 61

[illegible]


```

OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=URINARY BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
RT "Expression of ap2 gene in transitional epithelium of rabbit
   bladder.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF136241; AAD32209.1; -.
DR HSSP: P04117; ILID.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12536 MW; 4C19A538EC897F4F CRC64;

Query Match 46.3%; Score 329; DB 6; Length 113;
Best Local Similarity 56.2%; Pred. No. 3.5e-26;
Matches 63; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 11 WRLVDSKGFDEYKELGVGIALKMGAMAKPDCIITCDGKNLTKTESTLKTQFSCITLG 70
   :|||: ||:||||:||||: ||: ||||: ||: ||:||||:||||: ||: |||
Db 2 WKLVSENFDYKKEVGVGFATKRVAGMAPNMIISVNGDVITIKSESTPKNTEISPKLG 61

QY 71 EKFEETADGRKTQTYCNFTDGLVQHOEWGDKGKSTITRKLKDGKLVVECV 122
   :|||: ||| ||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: |||
Db 62 QEPDEVTADDRKSKSIITLDGGLVQVQKWDGKSTTIKRRKRGDKLVVECV 113

* RESULT 11
OS 057663 PRELIMINARY; PRT; 134 AA.
AC 057663;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
.DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-Isoform.
GN H6-FABP.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
   heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL: U92444; AAC60352.1; -.
DR HSSP: P10790; IBWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15182 MW; D4CRCFD50E131968 CRC64;

Query Match 46.1%; Score 327.5; DB 13; Length 134;
Best Local Similarity 46.5%; Pred. No. 6.1e-26;
Matches 60; Conservative 28; Mismatches 40; Indels 1; Gaps 1;

QY 4 VQOLEGRLVDSKGFDEYKELGVGIALKMGAMAKPDCIITCDGKN-LTIKTESPLKT 62
   :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: |||
Db 2 VERFVGTWKKMISSDNFDDYKALGVGFATQVGNRTKPNLVSVSDGQFFVCLKSQSTFKT 61

QY 63 TQFSCITLGEKFEETADGRKTQTYCNFTDGLVQHOEWGDKGKSTITRKLKDGKLVVECV 122
   :||: || ||||| ||||: ||| ||||| ||||: ||||: ||||: ||||: ||||: |||
```

```

Db 62 TEIKFKLNEPFEETADDRKTRTVVTLNGLKLVQKQWDCGKETNIERIEDGKLVAKCIM 121

QY 123 NNVTCTRIY 131
   :| | |
Db 122 GDVIAVRTY 130

RESULT 12
QY1896 PRELIMINARY; PRT; 135 AA.
ID 091896;
AC 091896;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
.DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Heart fatty acid binding protein.
GN H-FABP.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Teratani T., Nozawa R.;
RT "cDNA for heart fatty acid binding protein, from intron-1
   to exon-4.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Teratani T., Nozawa R.;
RT "The eel heart fatty acid binding protein.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039666; BAA92355.2; -.
DR EMBL: AB039665; BAA92355.2; JOINED.
DR EMBL: AB038695; BAA92241.3; -.
DR HSSP: P10790; IBWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; Lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
SQ SEQUENCE 135 AA; 15268 MW; 0FLCC8607D38F70B CRC64;

Query Match 45.9%; Score 326; DB 13; Length 135;
Best Local Similarity 47.4%; Pred. No. 8.8e-26;
Matches 64; Conservative 19; Mismatches 52; Indels 0; Gaps 0;

QY 1 MATVQQLGRWRLVDSKGFDEYKELGVGIALKMGAMAKPDCIITCDGKNLTIKTESTL 60
   :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: |||
Db 1 MVIMEPFLGTWHLKTSNFDYKELGVGFATRKIGNTTKPTLIIAADGDKFQVKTSLL 60

QY 61 KTTQFSCITLGEKFEETADGRKTQTYCNFTDGLVQHOEWGDKGKSTITRKLKDGKLVVECV 120
   :||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: |||
Db 61 KSTEINFKLGEFDEETADDRKRVKSVVVKLEDGKLVHLQKWDKSTSLVRAVDGKNKLTTL 120

QY 121 VMNVCTCTRIYKVE 135
   || ||||| |
Db 121 TFGNVVSTRHYRAE 135

RESULT 13
QYXS15 PRELIMINARY; PRT; 125 AA.
ID 09XS15;
AC 09XS15;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
.DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Heart-type fatty acid-binding protein (Fragment).
GN FABP3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RA SEQUENCE FROM N.A.
RA Schaap F.G., Pelsers M.M.A.L., van der Vusse G.J., Glatz J.F.C.;
RT "Cloning of equine H-FABP cDNA.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF143950; AAD32219.1; -
DR HSSP: P10790; IBWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1
DR PRINTS: PR00178; FATTYACIDBP.
FT NON_TER 1
SQ SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;

Query Match 45.0%; Score 320; DB 6; Length 125;
Best Local Similarity 49.6%; Pred. No. 3.3e-25;
Matches 61; Conservative 21; Mismatches 41; Indels 0; Gaps 0;

QY 11 WRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCITLG 70
   1:||||| ||:|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 1 WKLVDKSNFDYMKSLGVGFATRVANMTKPTTIIEVNGDTIITKTHSTFKNTEISFKLG 60
   1:||||| ||:|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

QY 71 EKEFEETADGRKTQTCVNFDTGALVHOEWGDKESITRKLKDGKLVVECMNNVTCTRI 130
   1:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 61 VEFDETTADDRKVKSLVTLDDGKLVHVOEWNGQETTLVRELIDGKLILTLTHGSVSTRT 120
   1:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

QY 131 YEK 133
   |||
Db 121 YEK 123
   |||

RESULT 14
QY18N9 PRELIMINARY; PRT; 132 AA.
AC QY18N9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Brain-type fatty-acid binding protein.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RA SEQUENCE FROM N.A.
RA Liu R.-Z., Denovan-Wright E.M., Wright J.M.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF448057; AAL40832.1; -
DR InterPro: IPR000463; Fatty_acid_BP.
DR Pfam: PF00061; lipocalin; 1
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1
DR PROSITE: PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 133 AA; 14882 MW; 91FB0400619A1926 CRC64;

Query Match 42.8%; Score 304; DB 13; Length 133;
Best Local Similarity 45.7%; Pred. No. 1.6e-23;
Matches 58; Conservative 24; Mismatches 45; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCIT 68
   1: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 7 GTWNLKESKNFEYMKIGVGGFATRVANMTKPTTIISKESGVFTLKTVSTFKSTEINFK 66
   1: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 69 LGEKFEETADGRKTQTCVNFDTGALVHOEWGDKESITRKLKDGKLVVECMNNVTCT 128
   1: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 67 LGEFEDETTADDRKVKSVITLDDGKLVHVKQWKGKETTLLREVSNNLTTLTIGDIVST 126
   1: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 129 RYKVE 135
   |||
Db 127 RHVKA 133
   |||

Search completed: November 25, 2002, 10:36:31
Job time : 30 secs
```

```
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RA SEQUENCE FROM N.A.
RA Schaap F.G., Pelsers M.M.A.L., van der Vusse G.J., Glatz J.F.C.;
RT "Cloning of equine H-FABP cDNA.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF143950; AAD32219.1; -
DR HSSP: P10790; IBWY.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1
DR PRINTS: PR00178; FATTYACIDBP.
FT NON_TER 1
SQ SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;

Query Match 45.0%; Score 320; DB 6; Length 125;
Best Local Similarity 49.6%; Pred. No. 3.3e-25;
Matches 61; Conservative 21; Mismatches 41; Indels 0; Gaps 0;

QY 11 WRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCITLG 70
   1:||||| ||:|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 1 WKLVDKSNFDYMKSLGVGFATRVANMTKPTTIIEVNGDTIITKTHSTFKNTEISFKLG 60
   1:||||| ||:|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

QY 71 EKEFEETADGRKTQTCVNFDTGALVHOEWGDKESITRKLKDGKLVVECMNNVTCTRI 130
   1:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 61 VEFDETTADDRKVKSLVTLDDGKLVHVOEWNGQETTLVRELIDGKLILTLTHGSVSTRT 120
   1:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

QY 131 YEK 133
   |||
Db 121 YEK 123
   |||

RESULT 14
QY18N9 PRELIMINARY; PRT; 132 AA.
AC QY18N9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Brain-type fatty-acid binding protein.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RA SEQUENCE FROM N.A.
RA Liu R.-Z., Denovan-Wright E.M., Wright J.M.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF448057; AAL40832.1; -
DR InterPro: IPR000463; Fatty_acid_BP.
DR Pfam: PF00061; lipocalin; 1
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1
DR PROSITE: PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 132 AA; 14918 MW; ED59506C71994C55 CRC64;

Query Match 44.0%; Score 313; DB 13; Length 132;
Best Local Similarity 48.8%; Pred. No. 1.8e-24;
Matches 60; Conservative 20; Mismatches 43; Indels 0; Gaps 0;

QY 11 WRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCITLG 70
   1:||||| ||:|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db 9 WKLVDKSNFDYMKSLGVGFATRVANMTKPTTIIEVNGDTIITKTHSTFKNTEISFKLG 68
   1:||||| ||:|||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

QY 71 EKEFEETADGRKTQTCVNFDTGALVHOEWGDKESITRKLKDGKLVVECMNNVTCTRI 130
   1:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:31:53 ; Search time 12 Seconds
(without alignments)
466.609 Million cell updates/sec

Title: US-09-788-074-3
Perfect score: 711
Sequence: 1 MATVQQLGRWRRLVDSKGF.....LVVECVNNVTCTRIYKVE 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	135	1	FABE_HUMAN
2	658	92.5	135	1	FABE_BOVIN
3	612	86.1	135	1	FABE_MOUSE
4	611	85.9	135	1	FABE_RAT
5	402	56.5	131	1	MYP2_RABIT
6	387	54.4	131	1	MYP2_HUMAN
7	382	53.7	131	1	FABA_BOVIN
8	382	53.7	131	1	MYP2_BOVIN
9	376	52.9	131	1	FABA_PIG
10	373	52.5	131	1	MYP2_MOUSE
11	371	52.2	131	1	FABA_SPETR
12	366	51.5	131	1	FABA_HUMAN
13	360	50.6	131	1	FABA_MOUSE
14	344	48.4	132	1	FABH_RAT
15	344	48.4	132	1	FABL_GINGI
16	343	48.2	132	1	FABH_SPETR
17	337	47.4	132	1	FABA_HUMAN
18	336	47.3	131	1	FABA_RAT
19	333	46.8	132	1	FABH_PIG
20	331	46.6	132	1	FABH_BOVIN
21	326	45.9	132	1	FABH_MOUSE
22	319	44.9	132	1	TLBP_RAT
23	318	44.7	132	1	TLBP_MOUSE
24	310	43.6	132	1	FABH_ONCMY
25	308	43.3	131	1	FABH_BOVIN
26	307	43.2	131	1	FABH_CHICK
27	304	42.8	131	1	FABH_MOUSE
28	303	42.6	131	1	FABH_HUMAN
29	303	42.6	131	1	FABH_RAT
30	286	40.2	114	1	FABL_LAMJA
31	222.5	31.3	133	1	FABP_ECHGR
32	214.5	30.2	137	1	RET3_HUMAN
33	212	29.8	136	1	RET3_MOUSE

34	210.5	29.6	137	1	RET3_XENLA
35	210	29.5	136	1	RET3_MOUSE
36	204.5	28.8	137	1	RET4_MOUSE
37	204	28.7	136	1	RET3_FUGRU
38	196	27.6	130	1	FABP_BLOTA
39	193	27.1	138	1	RET4_RAT
40	190.5	26.8	133	1	FABP_SCHMA
41	184	25.9	131	1	FABP_LEPDS
42	182	25.6	120	1	RET3_CHICK
43	178	25.0	134	1	RET1_RAT
44	174	24.5	134	1	RET1_HUMAN
45	172	24.2	134	1	RET1_MOUSE

ALIGNMENTS

RESULT 1
FABE_HUMAN STANDARD; PRT; 135 AA.
AC Q01469;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
DE fatty acid-binding protein homolog) (PA-FABP).
GN FABP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Keratinocytes;
RX MEDLINE=92381332; PubMed=1512466;
RA Madsen P.S., Rasmussen H.H., Leffers H., Honore B., Celis J.E.;
RT "Molecular cloning and expression of a novel keratinocyte protein
RT (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is
RT highly up-regulated in psoriatic skin and that shares similarity to
RT fatty acid-binding proteins.";
RL J. Invest. Dermatol. 99:299-305(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [4]
RP SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
RX MEDLINE=94379963; PubMed=8092987;
RA Siegenthaler G., Hotz R., Chatellard-Gruaz D., Didierjean L.,
RA Hellman U., Saurat J.-H.;
RT "Purification and characterization of the human epidermal fatty acid-
RT binding protein: localization during epidermal cell differentiation
RT in vivo and in vitro.";
RL Biochem. J. 302:363-371(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=99425110; PubMed=10493790;
RA Hohoff C., Borthers T., Rustow B., Spener F., van Tilbeurgh H.;
RT "Expression, purification and crystal structure determination of
RT recombinant human epidermal-type fatty acid-binding protein.";
RL Biochemistry 38:12229-12239(1999).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC C18 CHAIN LENGTH. DECREASING THE CHAIN LENGTH OR INTRODUCING

```
CC DOUBLE BONDS REDUCES THE AFFINITY. MAY BE INVOLVED IN KERATINOCYTE
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: KERATINOCYTES; HIGHLY EXPRESSED IN PSORIATIC
CC SKIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M94856; AAA58467.1; -
CC EMBL; BC019385; AAH19385.1; -
CC PDB; 1B56; 05-OCT-99.
CC Aarhus/Ghent-2DPAGE; 3007; IEF.
CC Genew; HGNC:3560; FABP5.
CC MIM; 605168; -
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding; 3D-structure.
CC KW TRANSPORT; 135 AA; 15164 MW; 77D38F8806143D63 CRC64;
CC SEQUENCE
CC -----
Query Match 100.0%; Score 711; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. NO. 6.9e-65;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATVQOLEGRWRLVDSKGFDEYNKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60
DB 1 MATVQOLEGRWRLVDSKGFDEYNKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60
[1]
QY 61 KTTQFSCITLGEKFEETADGRKTTQVCNFTDGLVQHQEWGDKGKESTITRKLKDGKLWVEC 120
DB 61 KTTQFSCITLGEKFEETADGRKTTQVCNFTDGLVQHQEWGDKGKESTITRKLKDGKLWVEC 120
[1]
QY 121 VMNNVTCTRIYEKVE 135
DB 121 VMNNVTCTRIYEKVE 135
[1]
RESULT 2
FABE_BOVIN STANDARD; PRT; 135 AA.
AC P5052; O62808;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Differentiation-
DE associated lipid binding protein LP2).
GN FABP5.
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-33 AND 116-129.
RC TISSUE=Lens;
RX JAWORSKI-97103094; PubMed=8947466;
RA Jaworski C., Mistow G.;
RT "LP2, a differentiation-associated lipid-binding protein expressed in
RT bovine lens.";
RL Biochem. J. 320:49-54(1996).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
```

```
RX MEDLINE=98198033; PubMed=9521644;
RA Kingma P.B., Bok D., Ong D.E.;
RT "Bovine epidermal fatty acid-binding protein: determination of ligand
RT specificity and cellular localization in retina and testis.";
RL Biochemistry 37:3250-3257(1998).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
CC THE UNSATURATED FATTY ACID PALMITATE (C16:0). MAY BE INVOLVED IN
CC THE UPTAKE AND TRANSPORT OF FATTY ACIDS ESSENTIAL FOR THE
CC NOURISHMENT OF THE SURROUNDING CELL TYPES. IT IS A POTENTIAL
CC TARGET FOR OXIDATIVE STRESS DURING CATARACT FORMATION IN LENS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LENS AND RETINA (FOUND IN THE
CC MUELLER CELLS), MODERATELY ABUNDANT IN HEART AND TESTIS (FOUND IN
CC THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U55188; AAB41297.1; -
CC EMBL; AF059507; AAC14711.1; -
CC HSSP; O01469; 1B56.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding; Phosphorylation.
CC KW MOD_RES 22 22 PHOSPHORYLATION (BY TYR-KINASES)
CC FT CONFLICT 52 52 L -> P (IN REF. 1).
CC FT SEQUENCE 135 AA; 15074 MW; 439B86AF88A34E2A CRC64;
CC -----
Query Match 92.5%; Score 658; DB 1; Length 135;
Best Local Similarity 91.9%; Pred. NO. 1.5e-59;
Matches 124; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 MATVQOLEGRWRLVDSKGFDEYNKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60
DB 1 MATVQQLVGRWRLVDSKGFDEYNKELGVGIALRKMGAMAKPDCIITSDGKNLSIKTESTL 60
[1]
QY 61 KTTQFSCITLGEKFEETADGRKTTQVCNFTDGLVQHQEWGDKGKESTITRKLKDGKLWVEC 120
DB 61 KTTQFSCITLGEKFEETADGRKTTQVCNFTDGLVQHQEWGDKGKESTITRKLKDGKLWVEC 120
[1]
QY 121 VMNNVTCTRIYEKVE 135
DB 121 VMNNVTCTRIYEKVE 135
[1]
RESULT 3
FABE_MOUSE STANDARD; PRT; 135 AA.
AC Q05816;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
DE fatty acid-binding protein homolog) (PA-FABP) (Keratinocyte lipid-
DE binding protein).
GN FABP5 OR MAL1 OR KLBP OR FABPE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```



```
CC C18 CHAIN LENGTH (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U13253; AAB86680.1; -.
CC EMBL; S69874; AAB30574.1; -.
CC EMBL; S83247; AAB46848.1; -.
CC HSP; Q01469; I856.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding.
CC KW CONFLICT 49 49 G -> N (IN REF. 1).
CC FT CONFLICT 112 112 K -> N (IN REF. 3).
CC SQ SEQUENCE 135 AA; 15059 MW; 978392433DF54358 CRC64;

Query Match 85.9%; Score 611; DB 1; Length 135;
Best Local Similarity 81.1%; Pred. No. 8.3e-55;
Matches 110; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 MATVQQLGRLVDSKGFDEYMKELGVGIALRKMGMAMKPCDIITCDGKNLTIKTESTL 60
Db 1 MASLKDLGKRLVSHESPFEDYMKELGVGLALRKMGMAMKPCDIITLDGNNLVKTESTV 60
QY 61 KTTQFSCTLGEKEPETTADGRKTQTVNFTDGLVQHQEWGDKESTITRKLKDGKLVVE 120
Db 61 KTVFVSCTLGEKDETTADGRKTETVCTFTDGLVQHQKWEKESTITRKLKDGKLVVE 120
QY 121 VMNVTCTRIYKVE 135
Db 121 VMNNAICTRIYKVVQ 135

RESULT 5
MYP2_RABIT STANDARD; PRT; 131 AA.
AC P02691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228063; PubMed=2453513;
RA Narayanan V., Barbosa E., Reed R., Tennekoon G.;
RT "Characterization of a cloned cDNA encoding rabbit myelin P2
RT protein.";
RL J. Biol. Chem. 263:8332-8337(1988).
RN [2]
RP SEQUENCE OF 1-55.
RX MEDLINE=80094496; PubMed=7356651;
RA Ishaque A., Hofmann T., Rhee S., Eylar E.H.;
RT "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT myelin.";
RL J. Biol. Chem. 255:1058-1063(1980).
RN [3]
RP SEQUENCE OF 55-131.
```

```
RX MEDLINE=82098098; PubMed=6172423;
RA Ishaque A., Hofmann T., Eylar E.H.;
RT "The complete amino acid sequence of the rabbit P2 protein.";
RL J. Biol. Chem. 257:592-595(1982).
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03744; AAA31451.1; -.
CC PIR; A03145; MPRB2.
CC PIR; A28081; A28081.
CC HSP; P02690; IPMP.
CC InterPro: IPR000463; Fatty_acid_BP.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Myelin; Lipid-binding; Transport; Acetylation.
CC KW INIT_MET 0 0 ACETYLATION.
CC FT MOD_RES 1 1
CC FT CONFLICT 72 72 E -> Q (IN REF. 3).
CC FT CONFLICT 83 83 I -> T (IN REF. 3).
CC FT CONFLICT 98 98 D -> N (IN REF. 3).
CC SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;

Query Match 56.5%; Score 402; DB 1; Length 131;
Best Local Similarity 61.1%; Pred. No. 9.6e-34;
Matches 77; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGMAMKPCDIITCDGKNLTIKTESTLKTQFSCT 68
Db 6 GTWKLVSSENFDDYMKALGVGLATRLKGLAKPNVIISKRGDIITRTTESTFKNTETSPK 65
QY 69 LGEKFEETTADGRKTQTVNFTDGLVQHQEWGDKESTITRKLKDGKLVVECVNNVTCT 128
Db 66 LGQEFETTADNRKTKSIITLGERGALNQVQKWDKETTIRKRLVDGKVMVVECKMGVVC 125
QY 129 RIYKVV 134
Db 126 RIYKVV 131

RESULT 6
MYP2_HUMAN STANDARD; PRT; 131 AA.
AC P02689;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92068191; PubMed=1720307;
RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;
RT "Isolation and sequence determination of cDNA encoding P2 protein of
```

```

RT human peripheral myelin.";
RL Biochem. Biophys. Res. Commun. 181:204-207(1991).
RN [2]
RP SEQUENCE.
RX MEDLINE=83058785; PubMed=6183401;
RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;
RT "The complete amino acid sequence of human P2 protein.";
RL J. Neurochem. 59:1759-1762(1982).
RN [3]
RP SEQUENCE OF 1-115 FROM N.A.
RX MEDLINE=95054012; PubMed=7525873;
RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
RT Tennekoon G.;
RP "Partial structure and mapping of the human myelin P2 protein gene.";
RL J. Neurochem. 63:2010-2013(1994).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D16181; BAA03726.1; -.
DR EMBL; D16179; BAA03726.1; JOINED.
DR EMBL; D16180; BAA03726.1; JOINED.
DR EMBL; X62167; CAA44096.1; -.
DR EMBL; S73470; AAB32592.2; -.
DR EMBL; S73468; AAB32592.2; JOINED.
DR EMBL; S73469; AAB32592.2; JOINED.
DR PIR; A03143; MP002.
DR PIR; J70977; J70977.
DR HSSP; P02690; 1PMP.
DR Genew; HGNC:9117; PMP2.
DR MIM; 170715; -.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLTATION.
FT DISULFID 117 124
FT CONFLICT 24 24
FT CONFLICT 98 98
FT CONFLICT 110 110
FT CONFLICT 110 110
SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;

Query Match 54.4%; Score 387; DB 1; Length 131;
Best Local Similarity 58.7%; Pred. No. 3 le-32;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVIALRMGAMAKPDCIITCDGKNLTIKTESTLTKTQFSCT 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKALCVGLATRLKGLNLAFTVIISKGDIIITRTSTFKNTEISFK 65

QY 69 LGKEPFEETADGRKTQTCVNFDTGALVQHQEWGDKESTITRKLKDGKLVVECVMMNVCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGQEFEEFTADNRKTSIVTFLQGSNLQVQRWDGKETTITKRLKLVGMVAECKMKGVVCT 125

QY 129 RYIEKV 134
Db 126 RYIEKV 131

```

```

RESULT 7
FABA_BOVIN STANDARD; PRT; 131 AA.
ID FABA_BOVIN STANDARD; PRT; 131 AA.
AC P48035;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
DE FAPB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96355299; PubMed=8702709;
RA Specht B., Bartezko N., Hohoff C., Kuhl H., Franke R.,
RA Boerchers T., Spener F.;
RT "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RL J. Biol. Chem. 271:19943-19949(1996).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89244; CAA61532.1; -.
DR HSSP; P04117; LLID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 19 19 PHOSPHORYLTATION (BY TYR-KINASES)
SQ SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;

Query Match 53.7%; Score 382; DB 1; Length 131;
Best Local Similarity 56.8%; Pred. No. 1e-31;
Matches 71; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVIALRMGAMAKPDCIITCDGKNLTIKTESTLTKTQFSCT 68
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 GTWKLVSSSENFDDYMKELGVGATRKVACMAKPTLIISLNGGVVTKSESTFKNTEISFK 65

QY 69 LGKEPFEETADGRKTQTCVNFDTGALVQHQEWGDKESTITRKLKDGKLVVECVMMNVCT 128
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 66 LGQEFEEFTADNRKTSIVNLDEGALVQVQNWGDKSTTIKRLKLMDDKMYLECVMGVCTAT 125

QY 129 RYIEKV 133
Db 126 RYIEKV 130

RESULT 8
MYP2_BOVIN STANDARD; PRT; 131 AA.
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;

```

DT	21-JUL-1986	(Rel. 01, Created)
DT	21-JUL-1986	(Rel. 01, Last sequence update)
DT	16-OCT-2001	(Rel. 40, Last annotation update)
DE	Myelin P2 protein.	
GN	PMP2.	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Bovidae; Bovinae; Bos.	
OX	NCBI_TaxID=9913;	
[1]		
RP	SEQUENCE.	
RX	MEDLINE=80225120;	PubMed=6156092;
KI	Kitamura K., Suzuki M., Suzuki A., Uyemura K.;	
RT	"The complete amino acid sequence of the P2 protein in bovine	
RT	peripheral nerve myelin.";	
RL	FEBS Lett. 115:27-30(1980).	
[2]		
RN	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).	
RX	MEDLINE=89005045;	PubMed=2458918;
KI	Jones T.A., Bergfors T., Sedzik J., Unge T.;	
RT	"The three-dimensional structure of P2 myelin protein.";	
RL	EMBO J. 7:1597-1604(1988).	
[3]		
RN	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).	
RX	MEDLINE=93253782;	PubMed=7683727;
KI	Cowan S.W., Newcomer M.E., Jones T.A.;	
RT	"Crystallographic studies on a family of cellular lipophilic	
RT	transport proteins. Refinement of P2 myelin protein and the structure	
RT	determination and refinement of cellular retinol-binding protein in	
RT	complex with all-trans-retinol.";	
RL	J. Mol. Biol. 230:1225-1246(1993).	
CC	-I- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN	
CC	CELLS.	
CC	-I- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER	
CC	CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN	
CC	PROTEIN.	
CC	-I- SIMILARITY: BELONGS TO THE FABP/P2/CRRBP/CRABP FAMILY OF	
CC	TRANSPORTERS.	
DR	PIR; A03144;	WPBO2.
DR	PDB; 1PMP;	26-JAN-95.
DR	InterPro; IPR000463;	Fatty_acid_BP.
DR	InterPro; IPR000566;	Lipocin_cytFABP.
DR	Pfam; PF00061;	LipoCalin; 1.
DR	PRINTS; PR00178;	FATTYACIDBP.
DR	PROSITE; PS00214;	FABP; 1.
KW	Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.	
FT	MOD_RES	1
FT	DISULFID	117 124
FT	SEQUENCE	131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;
QY	Query Match	53.7%; Score 382; DB 1; Length 131;
Db	Best Local Similarity	58.7%; Pred. No. le-31;
Db	Matches	74; Conservative 19; Mismatches 33; Indels 0; Gaps
QY	9 GRWRVLDSKGFDEYMKELGVGLAKMGAMAKPCDIITCDGKNLTITKTESPLKTTQFSCT	68
Db	: :	: :
QY	6 GTWKLVSSNFENFEYMKALCVGLATRKLNLAAPRVIIISKGDIIITRTSPFKMTLSFK	65
Db	:	:
QY	69 LGKFPEETTAGRKTQTVCNFTFDGALVQHODNGKESTITRKLKGDLKGLVECVNMNVTC	128
Db	:	:
QY	66 LGQEFETTADNRKTKSTVTLAGRSNLNQVKWNGNETTIKRKLVDGKWVYECKMKDVCT	125
Db	:	:
QY	129 RIYEKV	134
Db		
QY	126 RIYEKV	131
Db		
RESULT 9		
FABA_PIG		
ID	FABA_PIG	STANDARD; PRT; 131 AA.
AC	097788;	
DT	16-Oct-2001	(Rel. 40, Created)


```
RESULT 10
MYP2_MOUSE STANDARD; PRT; 131 AA.
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S39508; AAB19249.2; -.
CC PIR; JH0407; JH0407.
CC HSSP; P02690; 1PMP.
CC MGD; MGI:102667; Pmp2.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocin_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Myelin; Lipid-binding; Transport; Acetylation.
CC KW MYELIN; Lipid-binding; Transport; Acetylation.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
CC FT SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;
SQ
Query Match 52.5%; Score 373; DB 1; Length 131;
Best Local Similarity 55.6%; Pred. No. 8.1e-31;
Matches 70; Conservative 22; Mismatches 34; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
DB 6 GTWKLVSSSEHFDYMKALGVGLANRKLGNLAKPTVIISKKDYITIRTESAPKNTSEISFK 65
QY 69 LGKPEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDKGLVVECVNNVTCT 128
DB 66 LGGEFDETTADNRKAKSVITVLGRSLQKQKWDGKETAIRRTLLDGRMVVECIKMGVCT 125
QY 129 RYIEKV 134
DB 126 RYIEKV 131
RESULT 11
FABA_SPETR STANDARD; PRT; 131 AA.
AC Q99P60;
DT 15-JUN-2002 (Rel. 41, Created)
```

```
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP).
GN FABP4.
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Hittell D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding
RT proteins in hibernating ground squirrels.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF327855; AAK08084.1; -.
CC HSSP; P04117; ILID.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocin_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding; Phosphorylation.
CC KW TRANSPORT; Lipid-binding; Phosphorylation.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
CC FT SEQUENCE 131 AA; 14634 MW; FCEE7B092A2AF708 CRC64;
SQ
Query Match 52.2%; Score 371; DB 1; Length 131;
Best Local Similarity 55.2%; Pred. No. 1.3e-30;
Matches 69; Conservative 23; Mismatches 33; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
DB 6 GTWKLVSSSEHFDYMKELGVGIFATRVAGNAKPNMIISVNGDVITIRSESTFKNTSEISFK 65
QY 69 LGKPEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDKGLVVECVNNVTCT 128
DB 66 LGGEFDETTADNRKAKSVITVLGRSLQKQKWDGKSTTIKRRKREDDKLVECVKMGVTST 125
QY 129 RYIEKV 133
DB 126 RYIEKV 130
RESULT 12
FABA_HUMAN STANDARD; PRT; 131 AA.
AC P15090;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP).
GN FABP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90105397; PubMed=2481498;
RA Baxa C.A., Sha R.S., Buel M.K., Smith A.J., Matarese V.,
RA Chinander L.L., Boundy K.L., Bernlohr D.A.;
RT "Human adipocyte lipid-binding protein: purification of the protein
RL and cloning of its complementary DNA.";
RN Biochemistry 28:8683-8690(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Scrausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/FABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02874; AAA51689.1; -
DR EMBL: BC003672; AAH03672.1; -
DR PIR: A33363; A33363.
DR HSP: P04117; LLID.
DR Genew: HGNC:3559; FABP4.
DR MIM: 600434; -
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocin_cyFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;
SQ
Query Match 51.5%; Score 366; DB 1; Length 131;
Best Local Similarity 55.2%; Pred.No. 4.1e-30;
Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKGAMAKPDGCIITCDGKNLTIKTESTLTKTTFQSC 68
DB 6 GTWKLVSSEFDDYMKVEGVGATRKVACGMKPNMIISVNGDVITKSESTFKNTSFI 65
QY 69 LGEKPEETADRGKTQTVCNFTDGLVQHOEWGDKESTTRKLDGKLVVECMNVVTC 128
DB 66 LGQEFDEVTDARKVKSTITLDGGVLVHVQKWDGKSTTIKRRKEDDKLVVECMKGVTS 125
QY 129 RIVEK 133
DB 126 RYER 130
RESULT 13
FABA_MOUSE
ID FABA_MOUSE STANDARD; PRT; 131 AA.
AC P04117;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (FABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (P2 adipocyte protein) (Myelin P2 protein
DE homolog) (3T3-L1 lipid binding protein) (422 protein) (P15).
GN FABP4 OR AP2.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298159; PubMed=6206497;
RA Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.;
RT "Expression of specific mRNAs during adipose differentiation:
RL identification of an mRNA encoding a homologue of myelin P2
RT protein.";
RN Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233319; PubMed=3520554;
RA Hunt C.R., Ro J.H.-S., Dobson D.E., Min H.Y., Spiegelman B.M.;
RT "Adipocyte P2 gene: developmental expression and homology of
RT 5'-flanking sequences among fat cell-specific genes.";
RN Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278164; PubMed=3015943;
RA Phillips M., Djan P., Green H.;
RT "The nucleotide sequence of three genes participating in the adipose
RT differentiation of 3T3 cells.";
RN J. Biol. Chem. 261:10821-10827(1986).
RN [4]
RP SEQUENCE
RX MEDLINE=89008309; PubMed=2844775;
RA Matarese V., Bernlohr D.A.;
RT "Purification of murine adipocyte lipid-binding protein.
RT Characterization as a fatty acid- and retinoic acid-binding
RT protein.";
RN J. Biol. Chem. 263:14544-14551(1988).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [6]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=88203618; PubMed=2452440;
RA Cook J.S., Lucas J.J., Sibley E., Bolanowski M.A., Christy R.J.,
RA Kelly T.J. Jr., Lane M.D.;
RT "Expression of the differentiation-induced gene for fatty acid-binding
RT protein is activated by glucocorticoid and cAMP.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:2949-2953(1988).
RN [7]
RP SEQUENCE OF 10-131 FROM N.A.
RX MEDLINE=85105214; PubMed=3968175;
RA Cook K.S., Hunt C.R., Spiegelman B.M.;
RT "Developmentally regulated mRNAs in 3T3-adipocytes: analysis of
RT transcriptional control.";
RN J. Cell Biol. 100:514-520(1985).

```

RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=92207973; PubMed=1554730;
 RA Xu Z., Bernlohr D.A., Banaszak L.J.;
 RT "Crystal structure of recombinant murine adipocyte lipid-binding
 protein.";
 RL Biochemistry 31:3484-3492(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=93216758; PubMed=8463311;
 RA Xu Z., Bernlohr D.A., Banaszak L.J.;
 RT "The adipocyte lipid-binding protein at 1.6-A resolution. Crystal
 structures of the apoprotein and with bound saturated and unsaturated
 fatty acids.";
 RL J. Biol. Chem. 268:7874-7884(1993).
 CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
 CC CHAIN FATTY ACID AND RETINOIC ACID.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CBPP/CBAP FAMILY OF
 CC TRANSPORTERS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: K02109; AAA39416.1; -
 DR EMBL: M13264; AAA39870.1; -
 DR EMBL: M13261; AAA39870.1; JOINED.
 DR EMBL: M13262; AAA39870.1; JOINED.
 DR EMBL: M13263; AAA39870.1; JOINED.
 DR EMBL: M13385; AAA39417.1; -
 DR EMBL: AK003143; BAB22601.1; -
 DR EMBL: M20497; AAA37188.1; -
 DR EMBL: M28726; AAA37112.1; -
 DR PIR: A05089; A05089.
 DR PIR: A24884; A24884.
 DR PIR: A30810; A30810.
 DR PIR: B25952; B25952.
 DR PDB: 1ALB; 31-OCT-93.
 DR PDB: 1LIB; 30-APR-94.
 DR PDB: 1LIC; 30-APR-94.
 DR PDB: 1LID; 30-APR-94.
 DR PDB: 1LIE; 30-APR-94.
 DR PDB: 1LIF; 30-APR-94.
 DR PDB: 1ADL; 20-DEC-94.
 DR PDB: 1AB0; 16-JUN-97.
 DR PDB: 1ACD; 16-JUN-97.
 DR PDB: 1A18; 01-JUL-98.
 DR PDB: 1A2D; 01-JUL-98.
 DR SWISS-2DPAGE: P04117; MOUSE.
 DR MGD: MGI:98038; Fabp4.
 DR InterPro: IPR000463; Fatty_acid_BP.
 DR Pfam: PF000566; Lipoclin_cytFABP.
 DR Pfam: PF00061; lipocalin; 1.
 DR PRINTS: PS00178; FATTYACIDBP.
 DR PROSITE: PS00214; FABP; 1.
 KW Transport; Lipid-binding; Phosphorylation; 3D-structure.
 FT INIT_MET 0
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
 FT FT
 FT CONFLICT 39 39 (BY SIMILARITY).
 FT CONFLICT 110 110 N -> T (IN REF. 2; AAA39870).
 FT HELIX 2 4 G -> V (IN REF. 3; AAA39417).
 FT STRAND 6 14
 FT HELIX 16 23
 FT TURN 24 24
 FT TURN 27 35
 FT STRAND 39 45
 FT TURN 46 46

FT STRAND 48 54
 FT TURN 59 64
 FT TURN 66 67
 FT STRAND 70 73
 FT TURN 75 76
 FT STRAND 79 87
 FT TURN 88 89
 FT STRAND 90 97
 FT TURN 98 99
 FT STRAND 100 109
 FT TURN 110 111
 FT STRAND 112 119
 FT TURN 120 121
 FT STRAND 122 130
 SQ SEQUENCE 131 AA; 14519 MW; ED57D4E2774B8E32 CRC64;
 Query Match 50.6%; Score 360; DB 1; Length 131;
 Best Local Similarity 55.2%; Pred. No. 1.7e-29;
 Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTKTTESTLKTTFQSC 68
 Db 6 GTWKLVSSNFDDYMKVEGVGFATRKVAGMAKPNMIIISVNGDLVTIRSESTFKNTEISFK 65
 QY 69 LGEKFEETADGRKTQTVCFNFDGALVQHQEWGDKGKSTIRKLKDGKLVVECVNNVTCT 128
 Db 66 LGVEFDEITADRRKVKSIITLDGGALVQVQKWDGKSTIKRKRDKGLVVECVNMGVTST 125
 QY 129 RIVEK 133
 Db 126 RVIER 130
 RESULT 14
 FABH_RAT
 ID FABH_RAT STANDARD; PRT; 132 AA.
 AC P07483; Q9QY04;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fatty acid-binding protein, heart (H-FABP).
 GN FABP3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250640; PubMed=3036869;
 RA Heuckeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
 RT "Analysis of the tissue-specific expression, developmental
 RT regulation, and linkage relationships of a rodent gene encoding heart
 RT fatty acid binding protein.";
 RL J. Biol. Chem. 262:9709-9717(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88107756; PubMed=34271112;
 RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
 RT "Cloning and tissue distribution of rat heart fatty acid binding
 RT protein mRNA: identical forms in heart and skeletal muscle.";
 RL Biochemistry 26:7900-7904(1987).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=88153733; PubMed=3162235;
 RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;
 RT "Revision of the blocked N terminus of rat heart fatty acid-binding
 RT protein by liquid secondary ion mass spectrometry.";
 RL J. Biol. Chem. 263:4182-4185(1988).
 RN [4]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE=86250713; PubMed=2424895;
 RA Sacchetti J.C., Said B., Schulz H., Gordon J.I.;
 RT "Rat heart fatty acid-binding protein is highly homologous to the


```

FT MOD_RES 1 1 ACETYLLATION.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT MOD_RES 19 19 (POTENTIAL).
SQ SEQUENCE 132 AA; 15079 MW; 2AFDEA2C0BE2095F CRC64;

Query Match
Best Local Similarity 48.4%; Score 344; DB 1; Length 132;
Matches 66; Conservative 18; Mismatches 44; Indels 0; Gaps 0;

QY 4 VOQLEGRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKT 63
Db 1 VEAFLGSKLQKSHNFDEYMKNLDSLAQRKVATTVKPKTIISLDGDVITIKTESTFKST 60

QY 64 QFSCTLGEKFEETADGRKTQVCNFTDGLVQHOEWDGKESTITRKLKDGKLVVECVNM 123
Db 61 NIQFKLAEEFDETTADNRRTTKTVKLENGKLVQTORWDGKETTTLVRELQDGKLIILTCTMG 120

QY 124 NVTCTRIY 131
Db 121 DVVCTREY 128

```

Search completed: November 25, 2002, 10:35:30
Job time : 13 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:33:23 : Search time 17 Seconds
(without alignments)
763.420 Million cell updates/sec

Title: US-09-788-074-3

Perfect score: 711

Sequence: 1 MATVQQLGGRWRLVDSKGF.....LVVECMNVNVTTRYEKVE 135

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	135	2 I56326	fatty acid binding
2	612	86.1	135	2 A47497	lipid-binding prot
3	611	85.9	135	2 JC2201	fatty acid-binding
4	402	56.5	132	1 MPRB2	myelin P2 protein
5	387	54.4	132	1 MPBU2	myelin P2 protein
6	382	53.7	131	1 MPB02	myelin P2 protein
7	382	53.7	132	2 S57744	adipocyte-type fat
8	373	52.5	132	2 JH0407	myelin P2 protein
9	366	51.5	132	1 F2HUF	fatty acid-binding
10	358	50.4	132	2 B25952	myelin P2 protein
11	344	48.4	132	2 S20297	fatty acid-binding
12	344	48.4	133	2 A27452	fatty acid-binding
13	337	47.4	133	1 F2HUC	fatty acid-binding
14	331	46.6	133	2 A34676	fatty acid-binding
15	326	45.9	133	2 PC4011	fatty acid-binding
16	319	44.9	132	2 I52524	testis lipid bindi
17	308	43.3	131	2 S08479	fatty acid-binding
18	307	43.2	132	2 A49184	fatty acid-binding
19	304	42.8	132	2 I58161	lipid-binding prot
20	304	42.8	132	2 I48923	fatty acid-binding
21	303	42.6	132	2 I56510	fatty acid binding
22	234.5	33.0	135	2 T15205	hypothetical prote
23	231.5	32.6	137	2 T21203	hypothetical prote
24	224.5	31.6	136	2 T15207	hypothetical prote
25	214.5	30.2	138	1 RJHU2	retinoic acid-bind
26	212	29.8	137	1 RJHU1	retinoic acid-bind
27	210.5	29.6	138	2 A42495	retinoic acid-bind
28	210.5	29.6	138	2 I51265	xCRABP - African c
29	210	29.5	137	1 RJBOA	retinoic acid-bind

30	210	29.5	137	2 A35825	retinoic acid-bind
31	201.5	28.3	133	2 A48578	fatty acid-binding
32	193	27.1	139	2 I53298	cellular retinoic
33	190.5	26.8	133	2 A39818	14K fatty acid-bin
34	187.5	26.4	134	2 S29600	fatty acid-binding
35	178	25.0	135	1 RJRTO	retinol-binding pr
36	174	24.5	135	1 RJHU0	retinol-binding pr
37	172	24.2	135	2 S16355	retinol-binding pr
38	171	24.1	95	2 A61629	retinoic acid-bind
39	171	24.1	134	2 S43470	fatty acid-binding
40	168	23.6	133	2 A44870	fatty acid-binding
41	162	22.8	134	2 S69360	retinol-binding pr
42	159	22.4	134	2 S34717	retinol-binding pr
43	155	21.8	134	2 A29065	retinol-binding pr
44	154	21.7	100	2 S13796	retinoic acid-bind
45	153	21.5	132	2 I51450	fatty acid binding

ALIGNMENTS

RESULT 1

I56326

fatty acid binding protein homolog - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I56326

R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Cellis, J.E.

J. Invest. Dermatol. 99, 299-305, 1992

A>Title: Molecular cloning and expression of a novel keratinocyte protein (psoriasis-
ilality to fatty acid-binding proteins.

A:Reference number: I56326; MUID:92381332; PMID:1512466

A:Accession: I56326

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-135 <RES>

A:Cross-references: GB:M94856; NID:gl82353; PIDN:AAA58467.1; PID:gl82354

C:Genetics:

A:Gene: PA-FABP

C:Superfamily: myelin P2 protein

Query Match 100.0%; Score 711; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 4.4e-61;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATVQQLGGRWRLVDSKGFDEYMKELGVIALRKMGMARPDCCIITCDGKNLTKTESTL 60

|||||
Db 1 MATVQQLGGRWRLVDSKGFDEYMKELGVIALRKMGMARPDCCIITCDGKNLTKTESTL 60

QY 61 KTTQFSCTLGEKEFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLVEEC 120

|||||
Db 61 KTTQFSCTLGEKEFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLVEEC 120

QY 121 VMNNVTCTRIYEKVE 135

|||||
Db 121 VMNNVTCTRIYEKVE 135

RESULT 2

A47497

lipid-binding protein, keratinocyte - mouse

N:Alternate names: lipid-binding protein mall

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 13-Aug-1999

C:Accession: A47497; S36635

R:Krieg, P.; Fell, S.; Fuerstenberger, G.; Bowden, G.T.

J. Biol. Chem. 268, 17362-17369, 1993

A>Title: Tumor-specific overexpression of a novel keratinocyte lipid-binding protein.

A:Reference number: A47497; MUID:93352523; PMID:8349619

A:Accession: A47497

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <KRI>
A:Cross-references: EMBL:X70100; NID:g287985; PIDN:CAA49703.1; PID:g287986
C:Superfamily: myelin P2 protein

Query Match 86.1%; Score 612; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 1.4e-51;
Matches 108; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

QY 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60

Db 1 MASLKDEGKRWLVESHGFEYMKELGVGLALRKMAAMKPCDIITCDGNITIVKTSTV 60

QY 61 KTTQFSCITLGEKFEETADGRKTQTCVNETDGLVQHQEWGDKESIITRKLKDGKLVVVC 120

Db 61 KTTVFSCNLGEKFEETADGRKTETVCTFDGALVQHQWGDGKESIITRKLKDGKLVVVC 120

QY 121 VMNVVTCTRIYEKVE 135

Db 121 VMNNATCTRYEKVQ 135

RESULT 3

JC2201

fatty acid-binding protein, cutaneous - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Dec-2000

C:Accession: JC2201; JC7377

R:Watanabe, R.; Fujii, H.; Odani, S.; Sakakibara, J.; Yamamoto, A.; Ito, M.; Ono, T.

Biochem. Biophys. Res. Commun. 200, 253-259, 1994

A:Title: Molecular cloning of a cDNA encoding a novel fatty acid-binding protein from rat

A:Reference number: JC2201; MUID:94220094; PMID:8166694

A:Accession: JC2201

A:Molecule type: mRNA

A:Residues: 1-135 <KAT>

A:Cross-references: GB:S69874; NID:g546419; PTDN:AAB30574.1; PID:g546420

R:Odani, S.; Namba, Y.; Ishii, A.; Ono, T.; Fujii, H.

J. Biochem. 128, 355-361, 2000

A:Title: Disulfide bonds in rat cutaneous fatty acid-binding protein.

A:Reference number: JC7377

A:Contents: Skin

A:Accession: JC7377

A:Molecule type: mRNA

A:Residues: 1-135 <ODA>

C:Comment: This protein is involved in intracellular transport and metabolism of fatty a

F:22/Binding site: phosphate (Tyr) (covalent) (by insulin receptor/kinase) #status predi

C:Genetics:

A:Gene: c-fabp

C:Superfamily: myelin P2 protein

C:Keywords: cutaneous gland; disulfide bond; phosphoprotein; skin

F:109/Binding site: fatty acid (Arg) #status predicted

Query Match 85.9%; Score 611; DB 2; Length 135;

Best Local Similarity 81.5%; Pred. No. 1.7e-51;

Matches 110; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60

Db 1 MASLKDEGKRWLVESHGFEYMKELGVGLALRKMGAMAKPDCIITCDGNITIVKTSTV 60

QY 61 KTTQFSCITLGEKFEETADGRKTQTCVNETDGLVQHQEWGDKESIITRKLKDGKLVVVC 120

Db 61 KTTVFSCNLGEKFEETADGRKTETVCTFDGALVQHQWGDGKESIITRKLKDGKLVVVC 120

QY 121 VMNVVTCTRIYEKVE 135

Db 121 VMNNATCTRYEKVQ 135

RESULT 4

MPR2

myelin P2 protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999
A:Accession: A28081; A92266; A92372; A03145
R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.

J. Biol. Chem. 263, 8332-8337, 1988

A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.

A:Reference number: A28081; MUID:88228063; PMID:2453513

A:Accession: A28081

A:Molecule type: mRNA

A:Residues: 1-132 <NAR>

A:Cross-references: GB:J03744; NID:g165657; PTDN:AAA31451.1; PID:g165658

A:Note: translation of initiator Met is not shown

R:ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.

J. Biol. Chem. 255, 1058-1063, 1980

A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.

A:Reference number: A92266; MUID:80094496; PMID:7356651

A:Accession: A92266

A:Molecule type: protein

A:Residues: 2-56 <ISL>

R:ishaque, A.; Hofmann, T.; Eylar, E.H.

J. Biol. Chem. 257, 592-595, 1982

A:Title: The complete amino acid sequence of thr rabbit P2 protein.

A:Reference number: A92372; MUID:82098098; PMID:6172423

A:Accession: A92372

A:Molecule type: protein

A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction o

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/Disulfide bonds: #status predicted

Query Match 56.5%; Score 402; DB 1; Length 132;

Best Local Similarity 61.1%; Pred. No. 1.9e-31;

Matches 77; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTTOFSC 68

Db 7 GTWKLVSSENFDDYMKALGVGLATRLKGLNLPVLSKKGDIITRTSTFKNTSISK 66

QY 69 LGGEFETADGRKTQTCVNETDGLVQHQEWGDKESIITRKLKDGKLVVVCVMNVVTC 128

Db 67 LGGEFETADGRKTQTCVNETDGLVQHQEWGDKESIITRKLKDGKLVVVCVMNVVTC 126

QY 129 RYIEKV 134

Db 127 RYIEKV 132

RESULT 5

MPHU2

myelin P2 protein [validated] - human

A:Alternate names: peripheral myelin protein 2

C:Species: Homo sapiens (man)

C:Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000

C:Accession: J70977; A03143; S24224

R:Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human pe

A:Reference number: J70977; MUID:92068191; PMID:1720307

A:Accession: J70977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A:Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785; PMID:6183401

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98,'N',100-110,'D',112-132 <SUZ>

A;Description: Mammary derived growth inhibitor - not a distinct protein but a mix of he submitted to the EMBL Data Library, June 1995

A;Title: Human adipocyte lipid-binding protein: purification of the protein
A;Reference number: A33363; MUID:90105397; PMID:2481498

A;Description: Mammary derived growth inhibitor - not a distinct protein but a mix of he submitted to the EMBL Data Library, June 1995

C;Superfamily: myelin P2 protein
C;Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
F;1-133/product: fatty acid-binding protein #status experimental <NAT>
F;1/Modified site: acetylated amino end (Met) #status predicted

Query Match 48.4%; Score 344; DB 2; Length 133;
Best Local Similarity 52.8%; Pred. No. 6.9e-26;
Matches 66; Conservative 19; Mismatches 40; Indels 0; Gaps 0;

Qy 9 GRWLRLVDSKGFDEYMKELGVGIALRKMGAKAPDCIITCDGKNLTIKTESTLKTQFSCT 68
Dl :||| ||| ||| ||| ||| :||| ||| ||| :||| ||| ||| :||| ||| ||| :|||
Db 7 GTWKLVDKSNEDDYKMSLGVGFGATQVASMTKPTTIIIEKNGDTTITKHSFFKNTLSFQ 66
Dl :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 69 LGXKFETADTGRTQTVCNFPTDGLAVOHQEWDCKESTIRKKLDKGKLVCECVNNVTCT 128
Dl :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 LGVEFEVDTAADDRKVKSVTTLDGGKLVHVQKWDCQETTTLRELSDGKLILTLTHGNVVST 126
Dl :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 129 RIYEK 133
Dl :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 RYEK 131
Dl :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
FZHUO
fatty acid-binding protein, cardiac and skeletal muscle - human
N:Alternate names: fatty acid-binding protein 3 (FABP3)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence.revision 03-May-1996 #text_change 16-Jul-1999
C:Accession: S15432; JH0199; S00603; I54275; A27248
R:Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.
Biochem. J. 276, 203-207, 1991
A>Title: Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protein
A:Reference number: S15432; MUID:91248148; PMID:1710107
A:Accession: S15432
A:Molecule type: mRNA; protein
A:Residues: 1-133 <PRE>
A:Cross-references: EMBL:X56549; NID:g31292; PIDN:CAA39889.1; PID:g31293
R:Experimental source: heart muscle; skeletal muscle
R:Roelichers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.
Mol. Cell. Biochem. 98, 127-133, 1990
A>Title: Revision of the amino acid sequence of human heart fatty acid-binding protein
A:Reference number: JH0199; MUID:91094793; PMID:2266954
A:Accession: JH0199
A:Molecule type: protein
A:Residues: 2-129,'Q','131-133 <BOE>
R:Offner, G.D.; Brecher, P.; Sawilovich, W.B.; Costello, C.E.; Troxler, R.F.
Biochem. J. 252, 191-198, 1988
A>Title: Characterization and amino acid sequence of a fatty acid-binding protein from
A:Reference number: S00603; MUID:88339792; PMID:3421901
A:Accession: S00603
A:Molecule type: protein
A:Residues: 2-104,'K','106-124,'S','126-133 <OFF>
A>Note: submitted to the Protein Sequence Database, May 1988
R:Zanotti, G.; Scapin, G.; Spadon, P.; Veerkamp, J.H.; Sacchettini, J.C.
J. Biol. Chem. 267, 18541-18550, 1992
A>Title: Three-dimensional structure of recombinant human muscle fatty acid-binding p
A:Reference number: A49251; MUID:92406763; PMID:1526991
A:Contents: annotation: X-ray crystallography, 2.1 angstroms
A>Note: recombinant protein expressed in Escherichia coli
R:Troxter, R.F.; Offner, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Milunsky, A.; Wyan
Hum. Genet. 92, 563-566, 1993
A>Title: Localization of the gene for human heart fatty acid binding protein to chrom
A:Reference number: I54275; MUID:94085953; PMID:8262516
A:Accession: I54275
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 15-133 <RES>
A:Cross-references: GB:S67314; NID:g458861; PIDN:AAB29294.1; PID:g458862
C:Genetics:
A:Gene: GDB:FABP3
A:Cross-references: GDB:l28008; OMIM:134651
A:Map position: lp33-lp32
C:Superfamily: myelin P2 protein

Best Local Similarity 47.78; Pred. No. 1.2e-24;

Best Local Similarity 47.7%; Pred. No. 1.2e-24;

Qy 129 RIVEK 133

Qy 129 RIVEK 133

Db 127 RTYK 131

Search completed: November 25, 2002, 10:35:54
Job time : 18 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:35:18 ; Search time 10 Seconds
(without alignments)
211.430 Million cell updates/sec

Title: US-09-788-074-3
Perfect score: 711
Sequence: 1 MATVQQLGRLVDSKGF.....LVVCMNNVTCTRIYKVE 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	711	100.0	135	US-09-788-074-3
2	612	86.1	135	US-09-788-074-1
3	387	54.4	132	US-09-901-436A-11
4	366	51.5	132	US-09-905-235-1
5	337	47.4	132	US-09-986-240-2
6	337	47.4	133	US-09-901-436A-10
7	337	47.4	133	US-10-153-740-13
8	331	46.6	133	US-10-153-740-12
9	326	45.9	133	US-09-901-436A-7
10	326	45.9	133	US-10-153-740-11
11	303	42.6	132	US-09-971-187-2
12	291.5	41.0	131	US-10-153-740-15
13	223.5	31.4	149	US-09-925-302-496
14	214.5	30.2	138	US-09-736-457-328
15	195	27.4	160	US-09-925-301-848
16	174	24.5	135	US-09-901-436A-8
17	168	23.6	135	US-09-737-149-48
18	168	23.6	135	US-09-737-149-49
19	168	23.6	135	US-10-153-740-2

20	167	23.5	135	10	US-09-737-149-16	Sequence 16, Appl
21	136	19.1	156	10	US-09-737-149-14	Sequence 14, Appl
22	132	18.6	134	10	US-09-901-436A-9	Sequence 9, Appl
23	118	16.6	107	10	US-09-901-436A-2	Sequence 2, Appl
24	112.5	15.8	106	12	US-10-153-740-14	Sequence 14, Appl
25	110	15.5	70	10	US-09-737-149-46	Sequence 46, Appl
26	110	15.5	70	10	US-09-737-149-47	Sequence 47, Appl
27	94.5	13.3	127	9	US-09-981-353-21	Sequence 21, Appl
28	83	11.7	26	10	US-09-347-064-14	Sequence 14, Appl
29	76.5	10.8	98	10	US-09-925-299-1198	Sequence 1198, Ap
30	75	10.5	997	10	US-09-747-371-3	Sequence 3, Appl
31	73	10.3	758	10	US-09-903-248-2	Sequence 2, Appl
32	73	10.3	758	10	US-09-859-604-2	Sequence 2, Appl
33	73	10.3	758	10	US-09-903-063-2	Sequence 2, Appl
34	73	10.3	758	10	US-09-903-216-2	Sequence 2, Appl
35	73	10.3	758	10	US-09-903-199-2	Sequence 2, Appl
36	73	10.3	758	10	US-09-903-023-2	Sequence 2, Appl
37	69	9.7	343	10	US-09-815-242-5512	Sequence 5512, Ap
38	69	9.7	343	10	US-09-815-242-12152	Sequence 12152, A
39	69	9.7	1477	9	US-10-092-880-4	Sequence 4, Appl
40	68	9.6	614	10	US-09-782-051-2	Sequence 2, Appl
41	65.5	9.2	1426	10	US-09-912-020-340	Sequence 340, App
42	65	9.1	180	9	US-09-818-648-1	Sequence 1, Appl
43	65	9.1	180	10	US-09-828-217-1	Sequence 1, Appl
44	65	9.1	180	10	US-09-760-723-5	Sequence 5, Appl
45	65	9.1	180	10	US-09-355-925-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-788-074-3
; Sequence 3, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:
; APPLICANT: Hotamisligil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MAL1
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-074-3

Query Match	100.0%	Score 711;	DB 10;	Length 135;
Best Local Similarity	100.0%	Pred No. 1.3e-70;		
Matches 135;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MATVQQLGRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTKTESTL	60	
Db	1	MATVQQLGRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTKTESTL	60	
QY	61	KITQFSCITLGEKEFEETADGRKTQTCVNFDDGALVQHQEWGDKESTITRKLKDGKLWVEC	120	
Db	61	KITQFSCITLGEKEFEETADGRKTQTCVNFDDGALVQHQEWGDKESTITRKLKDGKLWVEC	120	
QY	121	VMNNVTCTRIYKVE 135		
Db	121	VMNNVTCTRIYKVE 135		

RESULT 2
US-09-788-074-1
; Sequence 1, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/10/153 740

APPLICATION NUMBER: 09/307,817

CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/10/153 740

```
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-740-12

Query Match          46.8%; Score 331; DB 12; Length 133;
Best Local Similarity 47.7%; Pred. No. 3.4e-29;
Matches 62; Conservative 23; Mismatches 45; Indels 0; Gaps 0;

QY 4 VOQLGRLVLVDSKGFDEYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLTKT 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 VDAFVGTKVLVDSKGFDDYMKSLGVGFATRQVGNMTPPTTIEVNGDVTVIKTQSTFKNT 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 64 QFSCITLGEFEETADGRKTQTVNCFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMN 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 EISFKLGVFEDETTADDRKVKSLVTLDDGGLVHVQKNGQETSILVRMDVGDKLLILTLHG 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 124 NVTCTRYEK 133
   | | | | |
Db 122 TAVCTRYEK 131
   | | | | |

RESULT 9
US-09-901-436A-7
; Sequence 7, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PF175D4
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-7

Query Match          45.9%; Score 326; DB 10; Length 133;
Best Local Similarity 48.8%; Pred. No. 1.2e-28;
Matches 61; Conservative 25; Mismatches 39; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLTKTQFSCT 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRQVASMTPKPTTIEKNGDVTITKTQSTFKNTINFQ 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 69 LGKFEETADGRKTQTVNCFTDGLVQHOEWGDKESTITRKLKDGKLVVECVNNVTCT 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 LGIEFEVTDADDRKVKSLVTLDDGGLVHVQKNGQETTLTRELVDGKLLILTLHGSVST 126
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 129 RYIEK 133
   | | | | |
Db 127 RYIEK 131
   | | | | |

RESULT 11
US-09-971-187-2
; Sequence 2, Application US/09971187
```

```
Db 127 RYIEK 131
   | | | | |

RESULT 10
US-10-153-740-11
; Sequence 11, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/153,740
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-153-740-11

Query Match          45.9%; Score 326; DB 12; Length 133;
Best Local Similarity 48.8%; Pred. No. 1.2e-28;
Matches 61; Conservative 25; Mismatches 39; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLTKTQFSCT 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 GTWKLVDKSNFDDYMKSLGVGFATRQVASMTPKPTTIEKNGDVTITKTQSTFKNTINFQ 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 69 LGKFEETADGRKTQTVNCFTDGLVQHOEWGDKESTITRKLKDGKLVVECVNNVTCT 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 LGIEFEVTDADDRKVKSLVTLDDGGLVHVQKNGQETTLTRELVDGKLLILTLHGSVST 126
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 129 RYIEK 133
   | | | | |
Db 127 RYIEK 131
   | | | | |

RESULT 11
US-09-971-187-2
; Sequence 2, Application US/09971187
```



```

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-328

Query Match          30.2%; Score 214.5; DB 9; Length 138;
Best Local Similarity 35.4%; Pred. No. 1.8e-16;
Matches 46; Conservative 36; Mismatches 41; Indels 7; Gaps 4;

QY 9 GRWLVDKSGFDYMKELGVGIALRK--MGAMAKPDCIITCDGKNLTIKTESTLKTTFPS 66
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 GNMKIIRSENFELLKVLGVNVMRLKIAVAASKPAVEIKQEGDTFYIKTSTTVRTTEIN 65

QY 67 CTLGKFEETADGRKTQTVCNF--TDCALVQHQ---EWDGKESTITRKL-KDGKLVVECV 121
   ||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 FKVGEEFEQTVDRCKSLVKWSENMVMCEQKLLKGEPKTSWPRELTNDGELITLWT 125

QY 122 MNNVTCTRIY 131
   ::|||::|
Db 126 ADDVVCTRYV 135

RESULT 15
US-09-925-301-848
; Sequence 848, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 848
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-848

Query Match          27.4%; Score 195; DB 10; Length 160;
Best Local Similarity 37.7%; Pred. No. 2.9e-14;
Matches 46; Conservative 25; Mismatches 45; Indels 6; Gaps 2;

QY 16 SKGFDYMKELGVGIALRK--MGAMAKPDCIITCDGKNLTIKTESTLKTTFQSCYLGKPF 73
Db 36 SENFDELLKALGVNMLRKVAVAASKPHVEIRQDGDQFYIKTSTTVRTTEINFKVGEGF 95
```

```

QY 74 EETTADGRKTQTVCNFTDCALVQHQ---EWDGKESTITRKLKDGKLVVECVNNTCTTR 129
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 96 EETVDGRKCRSLATWENENKIHCTQTLLLEGDPKTYWTRELANDELILTFGADDDVVCTR 155

QY 130 IY 131
   ||
Db 156 IY 157
   ||

Search completed: November 25, 2002, 10:37:10
Job time : 11 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:34:38 ; Search time 15 Seconds
(without alignments)
264.806 Million cell updates/sec

Title: US-09-788-074-3
Perfect score: 711
Sequence: 1 MATVQOEGRWRLVDSKGF.....LVCEVMNNVTCTRIYKVE 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	135	1	US-08-446-600A-4
2	387	54.4	132	1	US-08-409-731A-11
3	387	54.4	132	2	US-08-470-298B-11
4	387	54.4	132	2	US-09-023-073A-11
5	387	54.4	132	4	US-09-361-737-11
6	337	47.4	133	1	US-08-409-731A-10
7	337	47.4	133	2	US-08-470-298B-10
8	337	47.4	133	2	US-08-820-825-13
9	337	47.4	133	2	US-09-023-073A-10
10	337	47.4	133	4	US-09-307-817-13
11	337	47.4	133	4	US-09-361-737-10
12	337	47.4	133	4	US-09-734-036-13
13	331	46.6	133	2	US-08-820-825-12
14	331	46.6	133	4	US-09-307-817-12
15	331	46.6	133	4	US-09-734-036-12
16	326	45.9	131	1	US-08-409-731A-7
17	326	45.9	131	2	US-08-470-298B-7
18	326	45.9	133	2	US-08-820-825-11
19	326	45.9	133	2	US-09-023-073A-7
20	326	45.9	133	4	US-09-307-817-11
21	326	45.9	133	4	US-09-361-737-7
22	326	45.9	133	4	US-09-734-036-11
23	303	42.6	132	4	US-09-043-646-2
24	291.5	41.0	131	2	US-08-820-825-15
25	291.5	41.0	131	4	US-09-307-817-15
26	291.5	41.0	131	4	US-09-734-036-15
27	270	38.0	132	2	US-08-470-298B-12

28	214.5	30.2	138	1	US-08-468-709B-2	Sequence 2, Appli
29	214.5	30.2	138	2	US-08-241-664B-2	Sequence 2, Appli
30	214.5	30.2	138	5	PCT-US93-03936-2	Sequence 2, Appli
31	212	29.8	137	1	US-08-468-709B-4	Sequence 4, Appli
32	212	29.8	137	2	US-08-241-664B-4	Sequence 4, Appli
33	212	29.8	137	5	PCT-US93-03936-4	Sequence 4, Appli
34	210	29.5	137	1	US-08-468-709B-11	Sequence 11, Appl
35	210	29.5	137	2	US-08-241-664B-11	Sequence 11, Appl
36	204.5	28.8	138	1	US-08-468-709B-12	Sequence 12, Appl
37	204.5	28.8	138	2	US-08-241-664B-12	Sequence 12, Appl
38	190.5	26.8	133	1	US-08-554-463-1	Sequence 1, Appli
39	178	25.0	135	1	US-08-409-731A-8	Sequence 8, Appli
40	178	25.0	135	2	US-08-470-298B-8	Sequence 8, Appli
41	178	25.0	135	2	US-08-847-724-4	Sequence 4, Appli
42	174	24.5	135	2	US-08-847-724-6	Sequence 6, Appli
43	174	24.5	135	2	US-09-023-073A-8	Sequence 8, Appli
44	174	24.5	135	3	US-08-899-031-4	Sequence 4, Appli
45	174	24.5	135	4	US-09-361-737-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-446-600A-4
; Sequence 4, Application US/08446600A
; Patent No. 5719126
; GENERAL INFORMATION:
; APPLICANT: NO. 5719126dlund, James J. and Farooqui, Jamal Z.
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frost & Jacobs
; STREET: 2500 PNC Center, 201 East Fifth St.
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45202-4182
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,600A
; FILING DATE: 24 May 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,513
; FILING DATE: 24 No. 5719126ember 1992
; APPLICATION NUMBER: PCT/US93/11139
; FILING DATE: 16 No. 5719126ember 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann G. Robinson
; REGISTRATION NUMBER: 39,820
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 651-6128
; TELEFAX: (513) 651-6981
; TELEX: 21-4396 F&J Cln
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; US-08-446-600A-4

Query Match 100.0%; Score 711; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e-79;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATVQOEGRWRLVDSKGFDEYNKELGVGTALRKMGMAKPDCIITCDGKNLTIKTESTL 60

```
Db 1 MATVQLEGRWLVDKSGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTL 60
QY 61 KTFQSCITLGEKEEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVCC 120
Db 61 KTFQSCITLGEKEEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVCC 120
QY 121 VMNVVCTRIYKVE 135
Db 121 VMNVVCTRIYKVE 135

RESULT 2
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,731A
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PF175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORGANISM: MYELIN P2 (FIGURE 2)
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
US-08-409-731A-11

Query Match 54.4%; Score 387; DB 1; Length 132;
Best Local Similarity 58.7%; Pred. No. 7.8e-40;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVSSNFDDYMKALGVGLATRLKGLNLAKEPTVIISKGGDIITRTSTFKNTEISFK 66

QY 69 LGKEFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVCCVNNVTCT 128
Db 67 LGQEFETADNRKTKSVITLQSGSLNQVQWQDKETITRKLKLVNGKMAECKMKGVVCT 126

QY 129 RIYEKV 134
Db 127 RIYEKV 132

RESULT 3
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

```
US-08-470-298B-11
; Sequence 11, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
US-08-470-298B-11

Query Match 54.4%; Score 387; DB 2; Length 132;
Best Local Similarity 58.7%; Pred. No. 7.8e-40;
Matches 74; Conservative 19; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVSSNFDDYMKALGVGLATRLKGLNLAKEPTVIISKGGDIITRTSTFKNTEISFK 66

QY 69 LGKEFEETADGRKTQTVCNFTDGLVQHOEWGDKESTITRKLKDGKLVVCCVNNVTCT 128
Db 67 LGQEFETADNRKTKSVITLQSGSLNQVQWQDKETITRKLKLVNGKMAECKMKGVVCT 126

QY 129 RIYEKV 134
Db 127 RIYEKV 132

RESULT 4
US-09-023-073A-11
; Sequence 11, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```



```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-409-731A-10

Query Match          47.4%; Score 337; DB 1; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.le-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;

QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPPTTIEKNGDILTLKTHSTFKNTEISFK 66

QY 69 LGEKFEETTADGRKTQTVNCNFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMMNVCT 128
Db 67 LGVEFDETTADDRKVKSIIVTLDDGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTA VCT 126

QY 129 RYIEK 133
Db 127 RYIEK 131

RESULT 7
US-08-470-298B-10
; Sequence 10, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: FABP (FIGURE 2)
; US-08-470-298B-10
```

```
Query Match          47.4%; Score 337; DB 2; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.le-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
```

```
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPPTTIEKNGDILTLKTHSTFKNTEISFK 66

QY 69 LGEKFEETTADGRKTQTVNCNFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMMNVCT 128
Db 67 LGVEFDETTADDRKVKSIIVTLDDGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTA VCT 126

QY 129 RYIEK 133
Db 127 RYIEK 131

RESULT 8
US-08-820-825-13
; Sequence 13, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-820-825-13
```

```
Query Match          47.4%; Score 337; DB 2; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.le-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
```

```
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
Db 7 GTWKLVDKSNFDDYMKSLGVGFATQVASMTPPTTIEKNGDILTLKTHSTFKNTEISFK 66

QY 69 LGEKFEETTADGRKTQTVNCNFTDGLVQHOEWGDKESTITRKLKDGKLVVECVMMNVCT 128
Db 67 LGVEFDETTADDRKVKSIIVTLDDGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTA VCT 126

QY 129 RYIEK 133
Db 127 RYIEK 131
```


RESULT 9

US-09-023-073A-10
; Sequence 10, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,073A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF17502
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-073A-10

Query Match 47.4%; Score 337; DB 2; Length 133;
Best Local Similarity 51.2%; Pred. No. 1.1e-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTKTSTLKTTFQSC 68
Db 7 GTWKLVDKSNFDYMKSLGVGFATROVASMTPKPTTIIKNGDILTTLKTHSTFKNTEISFK 66
QY 69 LGKFEETADGKRTQTVCNFTDGLVQHQEWGDKESTITRKLDKGLVVECVMMNVCT 128
Db 67 LGVEFDETTADDRKVSIVTLDDGGLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCT 126
QY 129 RYIEK 133
Db 127 RYIEK 131

RESULT 10

US-09-307-817-13
; Sequence 13, Application US/09307817
; Patent No. 6232291
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,817
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,825
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-307-817-13

Query Match 47.4%; Score 337; DB 4; Length 133;

Best Local Similarity 51.2%; Pred. No. 1.1e-33;
Matches 64; Conservative 20; Mismatches 41; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMAMAKPDCIITCDGKNLTKTSTLKTTFQSC 68
Db 7 GTWKLVDKSNFDYMKSLGVGFATROVASMTPKPTTIIKNGDILTTLKTHSTFKNTEISFK 66
QY 69 LGKFEETADGKRTQTVCNFTDGLVQHQEWGDKESTITRKLDKGLVVECVMMNVCT 128
Db 67 LGVEFDETTADDRKVSIVTLDDGGLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCT 126
QY 129 RYIEK 133
Db 127 RYIEK 131

RESULT 11

US-09-361-737-10
; Sequence 10, Application US/09361737
; Patent No. 6287812
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

RESULT 12
US-09-734-036-13
; Sequence 13, Application US/09734036
; Patent No. 6413726
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,817
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.

```

```

RESULT 13
US-08-820-825-12
: Sequence 12, Application US/08820825
: Patent No. 5945309
: GENERAL INFORMATION:
: APPLICANT: NI, JIAN
: APPLICANT: YU, GUO-LIANG
: APPLICANT: GENTZ, REINER L.
: APPLICANT: DILLON, PATRICK
: TITLE OF INVENTION: CYTOSTATIN III
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HUMAN GENOME SCIENCES,
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0,
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/820,825-12
: FILING DATE: 19-MAR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOKES, ANDERS A.
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PF222
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 133 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-820-825-12

```

Query Match	46.6%	Score 331;	DB 2;	Length 133;
Best Local Similarity	47.7%	Pred. No. 5.8e-33;		
Matches	62;	Conservative 23;	Mismatches 45;	Indels 0; Gaps
Qy	4	VQQLGGRWRLVDSKGFDEYMKELGVGIALRKWKAMAKPDCILITCDGKNLTIKTESTLKTT	63	
Db	2	VDAFVGTVKWLVDKSNFDDYKMSLGVGFATRQGVNMTPTTIIIEVNGDVTIIIKTQSTFKRT	61	
Qy	64	QFSTLGEKFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKGLVVECVNM	123	
Db	62	EISFLGVEDETTADRRKKSIVTLDGKLVHVQKNGQETSLVREWDGKLIILTLTHG	121	
Qy	124	NVTCTRIYEK	133	
Db	122	TAVCTRIYEK	131	

```

RESULT 14
US-09-307-817-12
; Sequence 12, Application US/09307817
; Patent No. 6232291
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,817
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,825
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-307-817-12

```

```

Query Match      46.6%; Score 331; DB 4; Length 133;
Best Local Similarity 47.7%; Pred. No. 5.8e-33;
Matches 62; Conservative 23; Mismatches 45; Indels 0; Gaps
QY 4 VQOLEGRWRVLVDSKGFDEYKMKELGVGIARLKMAMAKPCIIICDGNKNIITKTESTLTT 63
Db VDAFVGTVTKLVDSKNFDDYMKSLGVGFATRGVGNMTKPTTIIIEVNGDVTIIKTKSTFKNT 61
QY 64 QFCSLTCEKEPEETIADGRKTQTVCNFTDGAIVGQHQWDGKSEITIRKLKDGKLVLVSCVNN 123

```

Search completed: November 25, 2002, 10:36:53
Job time : 16 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2002, 10:31:03 ; Search time 36 Seconds
(without alignments)
499.690 Million cell updates/sec

Title: US-09-788-074-3

Perfect score: 711

Sequence: 1 MATVQLGRRLVDSKGF.....LVVECMNNVTCTRIYKVE 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

```

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	135	AA055866	Melanogenic inhibi
2	711	100.0	135	AAU08674	Human keratinocyte
3	699	98.3	158	ABG27577	Novel human diagno
4	689	96.9	135	ABG61772	Novel fatty acid-b
5	624.5	87.8	134	AAU08666	Human NOV10 protei
6	619.5	87.1	163	AAU08665	Human NOV9 protei
7	612	86.1	135	AAU08673	Mouse keratinocyte
8	570.5	80.2	146	ABG60208	Human DITHP polype
9	452.5	63.6	172	AAU10059	Fatty acid-binding
10	430.5	60.5	181	ABG13617	Novel human diagno

11	375	52.7	136	19	AAW40227	Human myelin P2 pr
12	371	52.2	136	19	AAW40228	Bovine myelin P2 p
13	366	51.5	132	21	AAW90320	Human AFABP protei
14	366	51.5	132	23	ABB08076	Human ap2 protein.
15	360	50.6	132	21	AAW90319	Mouse AFABP protei
16	337	47.4	133	22	AAG66578	Human MDGI polypep
17	332	46.7	131	12	AAW13559	MDGI active peptid
18	331	46.6	133	22	AAG66577	Bovine MDGI polype
19	326	45.9	133	22	AAG66576	Mouse MDGI polypep
20	322.5	45.4	134	18	AAW31534	Porcine heart-fatt
21	304	42.8	132	16	AAW75423	Mouse cellular X b
22	303	42.6	132	18	AAW22408	Human cytostatin I
23	303	42.6	132	19	AAW80949	Amino acid sequenc
24	303	42.6	132	19	AAW81106	Human cytostatin I
25	303	42.6	132	20	AAW82403	Human cytostatin I
26	297	41.8	117	21	AAW03847	Human secreted pro
27	291.5	41.0	131	22	AAG66580	Human cytostatin I
28	291	40.9	132	21	AAW03957	Human secreted pro
29	269	37.8	522	22	ABG13615	Novel human diagno
30	253.5	35.7	130	22	ABG62690	Drosophila melanog
31	232.5	32.7	117	22	AAU30142	Novel human secret
32	230	32.3	433	22	ABG27578	Novel human diagno
33	223.5	31.4	149	21	AAW58158	Lung cancer associ
34	215	30.2	132	22	AAU10065	Cytostatin family
35	215	30.2	135	22	AAU10066	Cytostatin family
36	214.5	30.2	138	14	AAW42211	CRABP-II gene prod
37	214.5	30.2	138	22	AAW76852	Human lung tumour
38	214.5	30.2	138	23	AAU85507	Clone #19122 of lu
39	212	29.8	137	14	AAW42212	CRABP-I gene produ
40	200	28.1	88	21	AAW58740	Breast and ovarian
41	195	27.4	82	22	AAW75123	Human colon cancer
42	195	27.4	160	21	AAW43403	Human cancer assoc
43	190.5	26.8	133	16	AAW75643	Schistosoma manso
44	187.5	26.4	79	22	ABG13616	Novel human diagno
45	174	24.5	219	23	ABP41914	Human ovarian anti

ALIGNMENTS

```

RESULT 1
AA055866
ID  AA055866 standard; Protein; 135 AA.
XX
AC  AA055866;
XX
DT  07-DEC-1994 (first entry)
XX
DE  Melanogenic inhibitor.
XX
KW  Melanogenic inhibitor; MI; melanogenesis; melanin; pigment;
    depigmentation; melanoma.
XX
OS  Homo sapiens.
XX
PN  WO9412534-A.
XX
PD  09-JUN-1994.
XX
PF  16-NOV-1993; 93WO-US11139.
XX
PR  24-NOV-1992; 92US-0980513.
    01-SEP-1993; 93US-0115172.
XX
    (UYCI-) UNIV CINCINNATI.
XX
    Farooqui JZ, Nordlund JJ;
    WPI; 1994-200198/24.
    N-PSDB; AAQ66842.
XX
    Prodn. of a protein for inhibiting melanogenesis - useful for
    treating hyper-pigmentary diseases, destroying melanoma cells and

```

PT for lightening unwanted body hair
 PS Disclosure; Page 5; 40pp; English.
 XX
 CC PCR primers given in AA066843-44 were used to amplify RNA from
 CC human skin previously grafted onto nude mice, thereby providing
 CC DNA (AA066842) encoding melanogenic inhibitor protein (AAR55866).
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 711; DB 15; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1e-72;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKKMGAMAKPDCIITCDGKNTIKTESTL 60
 DB 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKKMGAMAKPDCIITCDGKNTIKTESTL 60
 QY 61 KTFQSCITLGERFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 DB 61 KTFQSCITLGERFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 QY 121 VMNVVTCRIYEKVE 135
 DB 121 VMNVVTCRIYEKVE 135
 RESULT 2
 AAU08674
 ID AAU08674 standard; Protein; 135 AA.
 AC AAU08674;
 DT 18-DEC-2001 (first entry)
 XX Human keratinocyte fatty acid binding protein, Mall.
 DE
 XX Human; Mal 1; keratinocyte fatty acid binding protein; anorectic;
 KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
 KW dyslipidaemia; atherosclerosis; antisense therapy.
 OS Homo sapiens.
 XX WO200160384-A1.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US05019.
 XX 17-FEB-2000; 2000US-0183106.
 XX (HARD) HARVARD COLLEGE.
 XX Hotamislilgil GS;
 XX WPI: 2001-570550/64.
 XX N-PSDB; AAS13247.
 PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidaemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor
 PS Disclosure; Page 2; 27pp; English.
 XX The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mal1 (keratinocyte
 CC fatty acid binding protein) or Mal1 activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
 CC useful for diagnosing these diseases. The present sequence is Human

CC Mal 1.
 XX Sequence 135 AA;
 Query Match 100.0%; Score 711; DB 22; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1e-72;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKKMGAMAKPDCIITCDGKNTIKTESTL 60
 DB 1 MATVQOEGRWRLVDSKGFDEYMKELGVGIALRKKMGAMAKPDCIITCDGKNTIKTESTL 60
 QY 61 KTFQSCITLGERFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 DB 61 KTFQSCITLGERFEETADGRKTQTVCNFTDGLVQHQEWGDKESTITRKLKDGKLWVEC 120
 QY 121 VMNVVTCRIYEKVE 135
 DB 121 VMNVVTCRIYEKVE 135
 RESULT 3
 ABG27577
 ID ABG27577 standard; Protein; 158 AA.
 XX AC ABG27577;
 XX 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #27568.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 WPI: 2001-639362/73.
 N-PSDB; AAS91764.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX Claim 20; SEQ ID No 57936; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABC00010-ABC30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 158 AA;

Query Match 98.3%; Score 699; DB 22; Length 158;
 Best Local Similarity 98.5%; Pred. No. 2.9e-71;
 Matches 133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATVQQLGRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60
 DB 24 MATVQQLGRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 83
 QY 61 KTTQFSCITLGEKFEETADGRKTQTVCNFTDGLVQHQEWGDKGKSTITRKLKDGKLVVEC 120
 DB 84 KTTQFSCITLGEKFEETADGRKTQTVCNFTDGLVQHQEWGDKGKSTITRKLKDGKLVVEC 143
 QY 121 VMNNVTCTRIYEKVE 135
 DB 144 VMNNVTCTRIYEKVE 158

RESULT 4
 ID ABG61772 standard; Protein; 135 AA.
 XX
 AC ABG61772;
 DT
 DT 14-AUG-2002 (first entry)
 XX
 DE Novel fatty acid-binding protein-like protein.
 XX
 KW Cancer; metabolic disorder; skin disorder; infectious disease; anorexia;
 KW behavioral disorder; valve disease; endocrine disorder; heart disorder;
 KW blood disorder; anxiety disorder; brain disorder; inflammatory disorder;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia;
 KW metabolic disturbance; obesity; metabolic syndrome X; wasting disorder;
 KW gene therapy; transgenic animal; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200229058-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31248.
 XX
 PR 05-OCT-2000; 2000US-238323P.
 PR 05-OCT-2000; 2000US-238325P.
 PR 06-OCT-2000; 2000US-238372P.
 PR 06-OCT-2000; 2000US-238373P.
 PR 06-OCT-2000; 2000US-238379P.
 PR 06-OCT-2000; 2000US-238382P.
 PR 06-OCT-2000; 2000US-238383P.
 PR 06-OCT-2000; 2000US-238384P.
 PR 06-OCT-2000; 2000US-238397P.
 PR 06-OCT-2000; 2000US-238400P.
 PR 06-OCT-2000; 2000US-238401P.
 PR 06-OCT-2000; 2000US-238402P.
 PR 14-MAR-2001; 2001US-275892P.
 PR 08-JUN-2001; 2001US-296860P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Taupier RJ, Burgess CE, Zerhusen BD, Mezes PS;
 PI Rastelli L, Malyankar UM, Grosse WM, Alsobrook JP, Lepley DM;
 PI Spytek KA, Li L, Edinger S, Gerlach V, Ellerman K, Macdougall J;

PI Gunther E, Millet I, Stone D, Smithson G, Szekeres ES;
 XX
 DR WPI: 2002-44103/47.
 DR N-PSDB; ABK92039.
 XX
 PT Novel isolated polypeptide, designated NOVX, useful for treating or
 PT preventing cancer, diabetes, obesity, dyslipidaemia, anorexia, and
 PT metabolic, neurodegenerative, immune and hematopoietic disorders -
 XX
 XX Claim 1; Page 42; 316pp; English.
 XX
 CC The invention describes an isolated polypeptide (I), useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease. (I), the polynucleotide encoding it (II) and an antibody
 CC (III) to (I) are useful for treating or preventing cancer, metabolic
 CC disorders, skin disorders, infectious disease, anorexia, behavioral
 CC disorders, valve diseases, endocrine disorders, heart and blood
 CC disorders, anxiety disorders, brain disorders, inflammatory disorders,
 CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
 CC immune disorders, haematopoietic disorders, and the various
 CC dyslipidaemias, metabolic disturbances associated with obesity, and the
 CC metabolic syndrome X and wasting disorders associated with chronic
 CC diseases. (I), (II) or (III) are useful in screening assays, detection
 CC assays (e.g., chromosomal mapping, tissue typing, forensic biology), and
 CC predictive medicine (e.g., diagnostic assays and prognostic assays), and
 CC in methods of treatment (e.g., therapeutic and prophylactic). (I) is
 CC useful as immunogen to produce antibodies immunospecific for (I), to
 CC screen for potential agonist and antagonist compounds, and as bait
 CC protein in a two-hybrid or three-hybrid assay. (II) is useful in gene
 CC therapy, to express (I), to detect (I) mRNA or a genetic lesion in a (I)
 CC gene, and to modulate activity of (I). A cell containing a vector
 CC expressing (I) is useful for producing non-human transgenic animals.
 CC This is the amino acid sequence of a novel human polypeptide described
 CC in the invention.
 XX
 SQ Sequence 135 AA;

Query Match 96.9%; Score 689; DB 23; Length 135;
 Best Local Similarity 95.6%; Pred. No. 3.2e-70;
 Matches 129; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATVQQLGRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60
 DB 1 MATVQQLGRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTL 60
 QY 61 KTTQFSCITLGEKFEETADGRKTQTVCNFTDGLVQHQEWGDKGKSTITRKLKDGKLVVEC 120
 DB 61 KTTQFSCITLGEKFEETADGRKTQTVCNFTDGLVQHQEWGDKGKSTITRKLKDGKLVVEC 120
 QY 121 VMNNVTCTRIYEKVE 135
 DB 121 VMNNVTCTRIYEKVE 135

RESULT 5
 AAU08666
 ID AAU08666 standard; Protein; 134 AA.
 XX
 AC AAU08666;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human NOV10 protein.
 XX
 KW Human; NOV10; cytostatic; nootropic; neuroprotective; vulneryary;
 KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
 KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
 KW antiatherosclerotic; dermatological; cancer; neurological disorder;
 KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
 KW immune disorder; autoimmune disease; respiratory disorder;
 KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
 KW cell growth regulation disorder; lesional psoriatic skin;
 KW atherosclerosis; abdominal aortic aneurysm.

XX	Homo sapiens.	Db	120 VTNNVTCTRIYKVE 134
OS			
XX			
PN	WO200168851-A2.		
XX			
PD	20-SEP-2001.		
XX			
PF	12-MAR-2001; 2001WO-US07735.		
XX			
PR	10-MAR-2000; 2000US-0188277.		
XX			
PR	10-MAR-2000; 2000US-0188316.		
PR	14-MAR-2000; 2000US-0189139.		
PR	14-MAR-2000; 2000US-0189140.		
PR	17-MAR-2000; 2000US-0190231.		
PR	17-MAR-2000; 2000US-0190401.		
XX			
XX	(CURA-) CURAGEN CORP.		
PA			
XX	Padigar M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;		
PI	Majumder K, Li L;		
XX			
XX	WPI: 2001-570869/64.		
DR	N-PSDB; AAS13344.		
DR			
XX			
XX	Novel polypeptides and nucleic acids homologous to members of collagen,		
PT	potassium channel, tuftelin family of proteins for diagnosing, treating		
PT	cancer, atherosclerosis, neurological, skin and enamel defect disorders		
PT			
PT			
XX			
PS	Claim 1; Page 37; 128pp; English.		
XX			
CC	The invention relates to isolated NOVX (NOVX1-11) polypeptides and		
CC	the polynucleotides that encode them. NOVX polypeptides, polynucleotides		
CC	and anti-NOVX antibodies are useful for treating or preventing a		
CC	pathology associated with NOVX polypeptide in humans and for treating a		
CC	syndrome associated with human disease e.g. disorders characterised by		
CC	altered cell motility, proliferation and migration e.g. cancer,		
CC	angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.		
CC	episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's		
CC	disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,		
CC	asthma, hypertension and seizure (NOV4), enamel defects, such as		
CC	amelogenesis imperfecta and disorders involving enamel defects,		
CC	including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic		
CC	neurological disorders, e.g. paraneoplastic limbic of brain-stem		
CC	encephalitis occurring during testicular cancer, diabetes, reproductive		
CC	health, metabolic and endocrine disorders, gastrointestinal disorders,		
CC	immune disorders and autoimmune diseases, respiratory disorders, bone		
CC	disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell		
CC	growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and		
CC	atherosclerosis, abdominal aortic aneurysm and neurological disorders		
CC	(NOV11). NOVX polypeptide is also useful for identifying an agent that		
CC	binds to it and a cell expressing NOVX polypeptide is useful for		
CC	identifying a therapeutic agent for use in treatment of a NOVX related		
CC	pathology. The antibodies and a polypeptide having 95% sequence identity		
CC	to NOVX polypeptide are useful for treating a pathological state in a		
CC	mammal. The present sequence represents NOV10, a possible epidermal		
CC	fatty acid-binding protein family member.		
XX			
SQ	Sequence 134 AA;		
	Query Match 87.8%; Score 624.5; DB 22; Length 134;		
	Best Local Similarity 88.9%; Pred. No. 6.7e-63;		
	Matches 120; Conservative 5; Mismatches 9; Indels 1; Gaps 1;		
QY	1 MATVQQLGGRWRVLVDSKGFDEYNKELGVGIALRKKMGAMAKPDCIITCDGKNLTIKTESTL 60		
DB	1 MATVQQLGGRWRVLVDSKGFDEYNKELGVGIALRKKMGAMAKPDCIITCDGKNLTIKTESTL 60		
QY	61 KTFQFSGTIGKEFEETADGRKTQTVCFNFTDGLVQHQEWQDGKESPIITRKLKDGKLIVVEC 120		
DB	61 KTFQFSGTIGKEFEETAGTAVGRKTQTVCFNFTDGLVQHQEWQDGKESPIITRKLKDGAS-VWDC 119		
QY	121. VMNNVTCTRIYKVE 135		

Db	120 VTNNVTCTRIYKVE 134
RESULT 6	
AAU08665	
ID	AAU08665 standard; Protein; 163 AA.
XX	
AC	AAU08665;
XX	
DT	18-DEC-2001 (first entry)
DE	Human NOV9 protein.
XX	
KW	Human; NOV9; cytostatic; nootropic; neuroprotective; vulnerary;
KW	cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
KW	antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW	antiatherosclerotic; dermatological; cancer; neurological disorder;
KW	Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW	immune disorder; autoimmune disease; respiratory disorder;
KW	bone disorder; musculoskeletal disorders; respiratory disorder;
KW	cell growth regulation disorder; lesional psoriatic skin;
KW	atherosclerosis; abdominal aortic aneurysm.
XX	
OS	Homo sapiens.
XX	
PN	WO200168851-A2.
XX	
PD	20-SEP-2001.
XX	
PF	12-MAR-2001; 2001WO-US07735.
XX	
PR	10-MAR-2000; 2000US-0188277.
PR	10-MAR-2000; 2000US-0188316.
PR	14-MAR-2000; 2000US-0189139.
PR	14-MAR-2000; 2000US-0189140.
PR	17-MAR-2000; 2000US-0190231.
PR	17-MAR-2000; 2000US-0190401.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Padigar M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;
PI	Majumder K, Li L;
XX	
XX	WPI: 2001-570869/64.
DR	N-PSDB; AAS13343.
DR	
XX	
XX	Novel polypeptides and nucleic acids homologous to members of collagen,
PT	potassium channel, tuftelin family of proteins for diagnosing, treating
PT	cancer, atherosclerosis, neurological, skin and enamel defect disorders
PT	
XX	
PS	Claim 9; Page 34; 128pp; English.
XX	
CC	The invention relates to isolated NOVX (NOVX1-11) polypeptides and
CC	the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC	and anti-NOVX antibodies are useful for treating or preventing a
CC	pathology associated with NOVX polypeptide in humans and for treating a
CC	syndrome associated with human disease e.g. disorders characterised by
CC	altered cell motility, proliferation and migration e.g. cancer,
CC	angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
CC	episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC	disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC	asthma, hypertension and seizure (NOV4), enamel defects, such as
CC	amelogenesis imperfecta and disorders involving enamel defects,
CC	including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
CC	neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC	encephalitis occurring during testicular cancer, diabetes, reproductive
CC	health, metabolic and endocrine disorders, gastrointestinal disorders,
CC	immune disorders and autoimmune diseases, respiratory disorders, bone
CC	disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC	growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
CC	atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC	(NOV11). NOVX polypeptide is also useful for identifying an agent that
CC	binds to it and a cell expressing NOVX polypeptide is useful for
CC	identifying a therapeutic agent for use in treatment of a NOVX related
CC	pathology. The antibodies and a polypeptide having 95% sequence identity
CC	to NOVX polypeptide are useful for treating a pathological state in a
CC	mammal. The present sequence represents NOV10, a possible epidermal
CC	fatty acid-binding protein family member.
XX	

PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiya MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI: 2002-383054/41.
DR N-PSDB; ABK71797.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics -
PS Claim 29; Page 679; 686pp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DTHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences
CC ABG9943-ABG60220 represent human DTHP polypeptides of the invention.
XX
XX Sequence 146 AA;
SQ
Query Match 80.2%; Score 570.5; DB 23; Length 146;
Best Local Similarity 81.4%; Pred. No. 1e-56; Indels 1; Gaps 1;
Matches 105; Conservative 16; Mismatches 7;
QY 1 MATVQOEGRWLRVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESYL 60
DB 6 MASLKDEGKRWLRVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITLDGNNLTIKTESIV 65
QY 61 KTFQFSGTGERFEETADGRKTQTCVNTDGLVQHQEWGDKESTITRKLKDGKLVVEC 120
DB 66 KTFVTSCTLGERFDETTADGRKTETVCTFTDGLVQHQEWGDKESTITRKLKDGKLVVEC 125
QY 121 VMNNV-TCT 128
DB 126 VMNNCPST 134
RESULT 9
AAU10059
ID AAU10059 standard; Protein; 172 AA.
XX
AC AAU10059;
XX
XX 14-FEB-2002 (first entry)
DE Fatty acid-binding family associated protein, NOV2.
XX
XX NOV: cytostatic; psoriasis; nootropic; neuroprotectant;
KW cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;
KW haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;
KW differentiation; proliferation; haematopoiesis; wound healing;
KW angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;
KW haemophilia; allergy; Pendered syndrome; skeletal dysplasia;
KW ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;
KW fatty acid-binding protein; FAPP; chromosome 5.
XX
OS Homo sapiens.
XX
XX WO200170978-A2.
PN
XX 27-Sep-2001.
PD

XX
PF
XX
PR 20-MAR-2001; 2001WO-US09093.
XX
PR 20-MAR-2000; 2000US-190768P.
PR 20-MAR-2000; 2000US-190835P.
PR 22-MAR-2000; 2000US-190972P.
PR 22-MAR-2000; 2000US-191199P.
PR 24-MAR-2000; 2000US-191947P.
PR 28-MAR-2000; 2000US-192657P.
PR 28-MAR-2000; 2000US-192664P.
PR 28-MAR-2000; 2000US-192665P.
PR 28-MAR-2000; 2000US-192984P.
PR 29-MAR-2000; 2000US-192836P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
PI Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
PI Vernet CAM;
XX
XX WPI: 2001-639127/73.
DR N-PSDB; AAS15722.
XX
XX Polypeptides and nucleic acids related to chloride channel,
PT insulin-like growth factor family of proteins, useful for diagnosing
PT and treating cancer, cystic fibrosis, acute pancreatitis and
PT Alzheimer's disease -
XX
PS Claim 1; Page 11; 151pp; English.
XX
XX The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX
CC polypeptides are useful for treating pathology associated with NOVX
CC polypeptide, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX, identifying agents binding to
CC NOVX and treatment of disorders associated with altered expression of
CC members of chloride channel-associated proteins e.g. cystic fibrosis and
CC congenital myotonia. NOVX proteins are useful in treatment of disorders
CC including psoriasis, cancer, diabetes, metabolic disorders of pancreas,
CC e.g. acute pancreatitis, abnormal growth and accumulation of mast cells
CC in one or more organs (e.g. haemophilia, anaemia). Pendered syndrome,
CC skeletal dysplasias, disorders characterised by altered cell shape,
CC motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial
CC disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the
CC treatment of disorders of vascular smooth muscle cell differentiation,
CC (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are
CC useful to screen for molecules which inhibit or enhance NOVX activity or
CC function and are useful as targets for the identifying small molecules,
CC that modulate or inhibit e.g. neurogenesis, proliferation, motility,
CC cell differentiation, haematopoiesis, wound healing and angiogenesis. NOV
CC sequences are also useful for: identifying a cell or tissue type in a
CC biological sample; amplifying DNA sequences from very small biological
CC samples e.g. hair or skin or body fluids and as primers and probes to
CC identify and/or clone NOVX homologues. NOVX proteins are useful
CC immunogens to generate antibodies to monitor protein levels and modulate
CC NOVX activity. Cells comprising the nucleic acids are useful for
CC producing transgenic animals, for studying the function and/or activity
CC of NOVX protein and identifying and/or evaluating modulators of NOVX
CC protein activity. This sequence is the NOV2 amino acid sequence (the gene
CC is located on chromosome 5) related to the fatty acid-binding protein
CC family proteins, one of 12 NOV polypeptides described in the method of
CC the invention.
XX
XX Sequence 172 AA;
SQ
Query Match 63.6%; Score 452.5; DB 22; Length 172;
Best Local Similarity 70.3%; Pred. No. 3.2e-43;
Matches 97; Conservative 11; Mismatches 25; Indels 5; Gaps 4;
QY 1 MATVQOEGRWLRVDSKGFDE--YMKELGVGIAL-RKMGAMAKPDCIITCDGKNLTIKTE 57
DB 37 MDTVQOEGRWLRVDSKGFDEYMKELGVGIALCKKMGAMAKKDCISFFDGNLTIKME 96
QY 58 STLKTTQFSCTLGEKFEETADGRKTQTCVNTDGLVQHQEWGDKESTITRKLKDGKLV 117
||||: | | ||:|||| ||||| | || | ||:|||| | ||||| |||

Db	97	STLKSYSFLRLRGKFFETTDGGRKQT-CFTTYGTLVRHOKWNGKEGKI-RKLKDRKL	154
Qy	118	VECVNNVTCTRIYKEV	135
		!::: :	
Db	155	VDCIINNVTCTRIYKEV	172
RESULT 10			
ABG13617			
ID	ABG13617	standard; Protein; 181 AA.	
XX	AC	ABG13617;	
XX	DT	18-FEB-2002 (first entry)	
XX		Novel human diagnostic protein #13608.	
XX		Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW		food supplement; medical imaging; diagnostic; genetic disorder.	
XX		Homo sapiens.	
OS	XX	WO200175067-A2.	
PN	XX	11-OCT-2001.	
PD	XX	30-MAR-2001; 2001WO-US08631.	
PF	XX	31-MAR-2000; 2000US-0540217.	
PR	XX	23-AUG-2000; 2000US-0649167.	
PR	XX	(HYSE-) HYSEQ INC.	
PA	XX	Drmanac RT, Liu C, Tang YT;	
PI	XX	WPI: 2001-639362/73.	
DR	XX	N-PSDB; AAS77804.	
DR	XX	New isolated polynucleotide and encoded polypeptides, useful in	
PT		diagnostics, forensics, gene mapping, identification of mutations	
PT		responsible for genetic disorders or other traits and to assess	
PT		biodiversity	
PS		Claim 20; SEQ ID NO 43976; 103pp; English.	
XX		The invention relates to isolated polynucleotide (I) and	
CC		polypeptide (II) sequences. (I) is useful as hybridisation probes,	
CC		polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC		and gene mapping, and in recombinant production of (II). The	
CC		polynucleotides are also used in diagnostics as expressed sequence tags	
CC		for identifying expressed genes. (I) is useful in gene therapy techniques	
CC		to restore normal activity of (II) or to treat disease states involving	
CC		(II). (II) is useful for generating antibodies against it, detecting or	
CC		quantitating a polypeptide in tissue, as molecular weight markers and as	
CC		a food supplement. (II) and its binding partners are useful in medical	
CC		imaging of sites expressing (II). (I) and (II) are useful for treating	
CC		disorders involving aberrant protein expression or biological activity.	
CC		The polypeptide and polynucleotide sequences have applications in	
CC		diagnostics, forensics, gene mapping, identification of mutations	
CC		responsible for genetic disorders or other traits to assess biodiversity	
CC		and to produce other types of data and products dependent on DNA and	
CC		amino acid sequences. ABG00010-ABG30377 represent novel human	
CC		diagnostic amino acid sequences of the invention.	
CC		Note: The sequence data for this patent did not appear in the printed	
CC		specification, but was obtained in electronic format directly from WIPO	
CC		at ftp.wipo.int/pub/published_pct_sequences.	
XX			
SQ		Sequence 181 AA;	
Query Match	60.58;	Score 430.5;	DB 22; Length 181;
Best Local Similarity	72.34;	Pred. No. 1.1e-40;	
Matches 99; Conservative	10; Mismatches 19;	Indels 9;	Gaps 8;

Qy	1	MATVQQLLEGRWRLVDSKGF--DEYMKELGVGIALRKMGAMAKPD-CIITCDGKNLT-IKTE	57			
Db	39	MAHVQQLLEGRWRLVDSKGFXXNTMKELGVLTIALRKMGRAQAQICITISDGNPSPLKTE	98			
Qy	58	SLTKTQFSCTL-GERFEETADGRKTQTVVC--NFTDGLVQHQEWG-KESTITRK-LK	112			
Db	99	SLTKTQFSCTLGKGFEEETADGQKKLTNCLSTFPDGLVQHQEWGDERKSTITRKNKX	158			
Qy	113	DGKLIV-VECVNNVTCT	128			
Db	159	DGEISWLECVNNVTCT	175			
RESULT 11						
AAW40227						
ID	AAW40227 standard; Protein; 136 AA.					
XX	AAW40227;					
XX	26-JUN-1998 (first entry)					
XX	Human myelin P2 protein.					
DE						
XX						
KW	Human; myelin; P2 protein; treatment; inflammatory polyneuritis;					
KW	Guillian-Barre syndrome; vasculitis; nerve inflammation;					
KW	gammopathy.					
XX						
OS	Homo sapiens.					
XX						
FH	Key Location/Qualifiers					
FT	Misc-difference 49					
FT	/note= "encoded by AAT"					
XX						
PN	WQ9803647-A2.					
XX						
PD	29-JAN-1998.					
XX						
XX	18-JUL-1997; 97WO-DE01535.					
PF						
XX						
PR	18-JUL-1996; 96DE-1029095.					
XX						
PA	(GOLD/) GOLD R.					
PA	(WEIS/) WEISHAUP T A.					
XX						
PI	Gold R, Weishaupt A;					
XX						
DR	WPI; 1998-120772/11.					
DR	N-PSDB; AAV10405.					
XX						
PT	Recombinant myelin proteins for treating T-cell mediated disease of					
PT	peripheral nervous system - by high dose antigen therapy, causing					
PT	apoptosis in T cells, for treating e.g. polyneuritis or					
PT	Guillian-Barre syndrome					
XX						
PS	Disclosure; Fig 4; 14pp; German.					
XX						
CC	The present sequence is the human myelin P2 protein, which can					
CC	be used to treat T-cell mediated diseases of the peripheral nervous					
CC	system, especially chronic-inflammatory polyneuritis,					
CC	Guillian-Barre syndrome, vasculitis and nerve inflammation in cases					
CC	of gammopathy.					
XX						
XX	Sequence 136 AA;					
Query Match 52.7%; Score 375; DB 19; Length 136;						
Best Local Similarity 57.3%; Pred. No. 1.5e-34;						
Matches 71; Conservative 20; Mismatches 33; Indels 0; Gaps						
Qy	9	GRWPLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT	68			
Db	7	GTWKLVSSEFNDDYMKALGVGIALRKLGNAKPTVIISKKGDIITRTSTFKNTEISFK	66			
Ov	69	LGKFEETADGRKTQTVCNFTDGLVQHQEWGKESTITRKLKDGKLVVQECVNNVTCT	128			

Db 67 LGQFEETTADNRKTKSVTLQRLSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 126
QY 129 RIVE 132
Db 127 RIVD 130

RESULT 12
AAW40228
ID AAW40228 standard; Protein; 136 AA.
XX AC AAW40228;
XX DT 26-JUN-1998 (first entry)
XX DE Bovine myelin P2 protein.
XX KW Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW Guillain-Barre syndrome; vasculitis; nerve inflammation;
KW gammopathy.
XX OS Bos taurus.
XX PN WO9803647-A2.
XX PD 29-JAN-1998.
XX PF 18-JUL-1997; 97WO-DE01535.
XX PR 18-JUL-1996; 96DE-1029095.
XX PA (GOLD/) GOLD R.
PA (WEIS/) WEISHAAPT A.
XX PI Gold R, Weishaupt A;
XX WPI; 1998-120772/11.

XX Recombinant myelin proteins for treating T-cell mediated disease of
PT peripheral nervous system - by high dose antigen therapy, causing
PT apoptosis in T cells, for treating e.g. polyneuritis or
PT Guillain-Barre syndrome
XX Disclosure; Fig 4; 14pp; German.
PS The present sequence is the bovine myelin P2 protein, which can
CC be used to treat T-cell mediated diseases of the peripheral nervous
CC system, especially chronic-inflammatory polyneuritis,
CC Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
CC of gammopathy.
XX SQ Sequence 136 AA;

Query Match 52.2%; Score 371; DB 19; Length 136;
Best Local Similarity 57.3%; Pred. NO. 4.2e-34;
Matches 71; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTSTLKTQFSCT 68
Db 7 GTWKLVSSENFDEYMKALGVGIALRKLGAKPPVILSKGDIITRTSPFKNTEISFK 66
QY 69 LGEKEFEETTADGRKTQTVCNFTDGLVQHOEWDGKRESTITRKLKDGKLVVECMNVCT 128
Db 67 LQCFEETADNRKTKSVTLQRLSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKDVVCT 126
QY 129 RIVE 132
Db 127 RIVD 130

RESULT 13
AA90320

ID AA90320 standard; Protein; 132 AA.
XX AC AA90320;
XX DT 22-NOV-2000 (first entry)
XX DE Human AFABP protein sequence.
XX KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
KW serum cholesterol; therapy; human.
XX OS Homo sapiens.
XX PN WO200047734-A1.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US03560.
XX PR 12-FEB-1999; 99US-0119880.
XX PA (HARD) HARVARD COLLEGE.
XX PI Lee M, Perrella MA, Hotamisligil GS;
XX WPI; 2000-506094/45.
XX N-PSDB; AAA37717.
XX Reducing expression of adipocyte fatty acid binding protein through
PT administration of a compound is used to inhibit formation of an
PT atherosclerotic lesion -
XX Disclosure; Page 14; 43pp; English.

XX This sequence represents the human AFABP (adipocyte fatty
CC acid binding protein) protein sequence. The invention relates to a method
CC for inhibiting formation of an atherosclerotic lesion comprising
CC administering to a mammal a compound that reduces expression of adipocyte
CC fatty acid binding protein (AFABP). The method is used to inhibit
CC formation of atherosclerotic lesions. The method is used to identify
CC compounds which can be used to inhibit formation of atherosclerotic
CC lesions through inhibition of AFABP binding to an intracellular ligand
CC in a macrophage or adipocyte, inhibition of development of an
CC atherosclerotic lesion, inhibition of a macrophage differentiating into
CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity
CC may be inhibited to treat atherosclerosis or to treat individuals at risk
CC of developing atherosclerosis. Inhibiting AFABP expression or activity
CC reduces the development of atherosclerotic lesions despite a high level
CC of serum cholesterol.

XX SQ Sequence 132 AA;

Query Match 51.5%; Score 366; DB 21; Length 132;
Best Local Similarity 55.2%; Pred. NO. 1.5e-33;
Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 9 GRWLVDKSGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTSTLKTQFSCT 68
Db 7 GTWKLVSSENFDEYMKGVGATRKVAGMAKPNMIISYNGDVITIKSESTFKNTEISFI 66
QY 69 LGEKEFEETTADGRKTQTVCNFTDGLVQHOEWDGKRESTITRKLKDGKLVVECMNVCT 128
Db 67 LQCFEETADNRKTKSVTLQRLSLNQVQWMDGKRETTIKRKLVLNGKMAECKMKGVVCT 126
QY 129 RIVE 133
Db 127 RIVER 131

RESULT 14
ABB08076
ID ABB08076 standard; protein; 132 AA.

```

XX AC ABB08076;
XX DT 10-SEP-2002 (first entry)
XX DE
XX KW Human ap2 protein.
XX DE
XX KW ap2; antiarteriosclerotic; cardiant; cerebroprotective; antianginal;
XX KW cytosolic protein; adipocyte; HMG CoA reductase; pravastatin; human.
XX OS Homo sapiens.
XX PN US2002035064-A1.
XX PD 21-MAR-2002.
XX PF 13-JUL-2001; 2001US-0905235.
XX PR 17-SEP-1998; 98US-100677P.
XX PR 07-SEP-1999; 99US-0390275.
XX PA (ROBL/) ROBL J A.
XX PA (PARK/) PARKER R A.
XX PA (BILL/) BILLER S A.
XX PA (JAMI/) JAMIL H.
XX PA (JACO/) JACOBSON B L.
XX PA (KODU/) KODUKULA K.
XX PI Robl JA, Parker RA, Biller SA, Jamil H, Jacobson BL, Kodukula K;
XX WPI: 2002-470589/50.
XX
XX PT Method useful for treatment of e.g. atherosclerosis, myocardial
XX PT infarction, angina involves administering ap2 inhibitor e.g.
XX PT (2'-(4,5-diphenyl-oxazol-2-yl)-biphenyl-3-yloxy)-acetic acid -
XX PS Disclosure; Page 16; 26pp; English.
XX
XX CC The invention relates to the treatment of atherosclerosis which involves
XX CC administering an ap2 inhibitor or a combination of an ap2 inhibitor and
XX CC another type antiatherosclerotic agent, for example, an HMG CoA reductase
XX CC inhibitor such as pravastatin. The method is used for treating
XX CC atherosclerosis; for preventing, inhibiting or reducing risk of
XX CC cardiovascular disorders e.g. cardiac and/or cerebral ischaemia,
XX CC myocardial infarction, angina, peripheral vascular disease and stroke.
XX CC The present sequence represents the amino acid sequence of human ap2
XX CC protein, a cytosolic protein present in adipocytes.
XX SQ Sequence 132 AA;
    Query Match 51.5%; Score 366; DB 23; Length 132;
    Best Local Similarity 55.2%; Pred. No. 1.5e-33;
    Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
DB 7 GTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVIITKSESTFKNTEISFI 66
QY 69 LGKEFETTTADGRKTQTCVNFDTGALVHOEWDPGKESTITRKLDGKLVVCEVMNNVTCT 128
DB 67 LGGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRRKREDDKLVVCEVMKGVST 126
QY 129 RYIEK 133
DB 127 RYVER 131

```

RESULT 15

AAY90319

ID. AAY90319 standard; Protein; 132 AA.

XX

AC AAY90319;

XX

```

DT 22-NOV-2000 (first entry)
XX DE Mouse AFABP protein sequence.
XX KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
XX KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
XX KW serum cholesterol; therapy; mouse.
XX OS Mus sp.
XX PN WO200047734-A1.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US03560.
XX PR 12-FEB-1999; 99US-0119880.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Lee M, Perrella MA, Hotamisligil GS;
XX WPI: 2000-506094/45.
XX N-PSDB; AAA37716.
XX
XX PT Reducing expression of adipocyte fatty acid binding protein through
XX PT administration of a compound is used to inhibit formation of an
XX PT atherosclerotic lesion -
XX PS Disclosure; Page 14; 43pp; English.
XX
XX CC This sequence represents the mouse AFABP (adipocyte fatty
XX CC acid binding protein) protein sequence. The invention relates to a method
XX CC for inhibiting formation of an atherosclerotic lesion comprising
XX CC administering to a mammal a compound that reduces expression of adipocyte
XX CC fatty acid binding protein (AFABP). The method is used to inhibit
XX CC formation of atherosclerotic lesions. The method is used to identify
XX CC compounds which can be used to inhibit formation of atherosclerotic
XX CC lesions through inhibition of AFABP binding to an intracellular ligand
XX CC in a macrophage or adipocyte, inhibition of development of an
XX CC atherosclerotic lesion, inhibition of a macrophage differentiating into
XX CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity
XX CC may be inhibited to treat atherosclerosis or to treat individuals at risk
XX CC of developing atherosclerosis. Inhibiting AFABP expression or activity
XX CC reduces the development of atherosclerotic lesions despite a high level
XX CC of serum cholesterol.
XX SQ Sequence 132 AA;
    Query Match 50.6%; Score 360; DB 21; Length 132;
    Best Local Similarity 55.2%; Pred. No. 7.2e-33;
    Matches 69; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 9 GRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTQFSCT 68
DB 7 GTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVIITKSESTFKNTEISFK 66
QY 69 LGKEFETTTADGRKTQTCVNFDTGALVHOEWDPGKESTITRKLDGKLVVCEVMNNVTCT 128
DB 67 LGVEFDEVTADDRKVKSTITLDGGALVQVQKWDGKSTTIKRRKRDGKLVVCEVMKGVYST 126
QY 129 RYIEK 133
DB 127 RYVER 131

```

Search completed: November 25, 2002, 10:35:11

Job time : 37 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:24:47 ; Search time 87.5 Seconds
(without alignments)
6023.640 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 2239
Sequence: 1 aatgggagcaactgctagc.....tctatgagaagtgcattga 1279

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DBV=xlp
-Q/cgn2_1/USPTO.spool/US09788074/runat_25112002_093514_15675/app_query.fasta_1.1415
-DB-SPTREMBL_21 -ONFT-fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=diplom62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09788074.ecgn_1.124.@runat_25112002_093514_15675 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL_21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rviro:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	183.5	8.2	132 13 Q90X55	Q90x55 gallus gall

2	180	8.0	132 13 Q90W92	Q90w92 fundulus he
3	179.5	8.0	113 6 Q9XSG4	Q9xsg4 oryctolagus
4	176.5	7.9	99 6 Q97675	Q97675 sus scrofa
5	171.5	7.7	132 13 Q8QHA8	Q8qha8 anser anser
6	169.5	7.6	86 13 Q8UWD3	Q8uwd3 anser anser
7	168.5	7.5	132 11 Q9DAK4	Q9dak4 mus musculus
8	165.5	7.4	125 6 Q9XSI5	Q9xsi5 equus caball
9	160.5	7.2	111 13 Q90ZG6	Q90z96 brachydanio
10	159.5	7.1	166 4 Q9H047	Q9h047 homo sapien
11	157.5	7.0	97 11 Q9QV90	Q9qv90 mus sp. lng
12	155	6.9	53 13 Q9QW19	Q9qw19 gallus gall
13	155	6.9	134 13 Q9W653	Q9w653 gobionototh
14	154.5	6.9	132 13 Q918N9	Q918n9 brachydanio
15	152	6.8	134 13 Q97663	Q97663 nototenha
16	152	6.8	134 13 Q97691	Q97691 cryodraco a
17	151.5	6.8	133 13 Q8UWG7	Q8uvw7 brachydanio
18	151.5	6.8	150 11 Q9R290	Q9r290 rattus norv
19	150	6.7	134 13 Q97666	Q97666 paracheanic
20	148	6.6	135 13 Q91896	Q91896 anguilla ja
21	147	6.6	133 13 Q97669	Q97669 nototenha
22	146	6.5	133 13 Q97667	Q97667 chaenoceph
23	146	6.5	133 13 Q97668	Q97668 cryodraco a
24	146	6.5	133 13 Q97670	Q97670 gobionototh
25	143.5	6.4	136 5 Q8WR15	Q8wr15 metapeneus
26	138.5	6.2	132 11 Q9DAL2	Q9dal2 mus musculu
27	138	6.2	100 13 Q97664	Q97664 rhigophila
28	137	6.1	132 5 Q9UIG6	Q9uig6 fasciola he
29	126	5.6	136 5 Q91814	Q91814 caenorhabdi
30	125	5.6	114 11 Q99M00	Q99m00 mus musculu
31	124	5.5	114 11 Q9VGM2	Q9vgm2 drosophila
32	117	5.2	133 5 Q9BWK1	Q9bmk1 echinococcu
33	117	5.2	133 5 Q9BLY5	Q9bly5 echinococcu
34	117	5.2	133 5 Q967X3	Q967x3 echinococcu
35	114	5.1	135 5 Q91812	Q91812 caenorhabdi
36	113	5.0	147 13 Q9PSA5	Q9psa5 xenopus lae
37	112	5.0	132 5 Q45035	Q45035 schistosoma
38	110	4.9	132 5 Q9BME8	Q9bme8 schistosoma
39	110	4.9	132 5 Q26517	Q26517 schistosoma
40	109	4.9	98 5 Q8T5U8	Q8t5u8 schistosoma
41	109	4.9	132 5 Q61236	Q61236 schistosoma
42	109	4.9	133 5 Q8T5U9	Q8t5u9 manduca sex
43	108	4.8	128 13 Q919A9	Q919a9 lygodactylu
44	103	4.6	126 5 Q94567	Q94567 fasciola g1
45	103	4.6	132 5 Q9UAS2	Q9uas2 fasciola g1

ALIGNMENTS

RESULT 1
Q90X55 PRELIMINARY; PRT; 132 AA.
ID AC Q90X55; Q90X56;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Adipocyte fatty acid binding protein.
GN AFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Wang Q., Ao J., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Study on chicken AFABP gene as candidate gene for fatness trait.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene

```
RT in chicken.*;
RN Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene
in chicken.*;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432507; AAL30744.2; -
DR EMBL; AF432506; AAL30743.1; -
DR InterPro; IPR000463; Fatty_acid_BP
DR InterPro; IPR000566; Lipocin_cyFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PROSITE; PS00214; FABP; UNKNOWN_1.
SQ SEQUENCE 132 AA; 14894 MW; 4f5905FAB8DA268B CRC64;

Alignment Scores:
Pred. No.: 5,41e-12 Length: 132
Score: 183.50 Matches: 51
Percent Similarity: 33.17% Conservative: 16
Best Local Similarity: 25.25% Mismatches: 25
Query Match: 8.20% Indels: 110
DB: 13 Gaps: 1

US-09-788-074-2 (1-1279) x Q90W92 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACGACTGTATCATTCAGC 190
DB 25 GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer 44
QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACGACGACTGAAGCAGCTGTCTCTCT 250
DB 45 IleAsnGlyAspValIleThrIleArgSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGATTGTATGAACACGACGACTGTGCGCAAGAACTGAGGTCAGC 310
DB 65 PheLysLeuGlyGluPheAspGluThrThrAlaAspArgLysThr-LysAsn-- 83
QY 311 TACAACATACTGTGAAGCGACAGAACTTCTAGATTTTACAGATTAAATTCATTAAACAAT 370
DB 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
DB 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
DB 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
DB 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGGTCTGGGGGTCTTCTTCACTTTGGAAGATCATCAAC 610
DB 83 ----- 83
QY 611 TAACACCCTGTATTTTTCGACAGCGTCTGCACCTTCCAAAGCGGTGCCCTGTCTCAGCA 670
DB 84 ----- 84
QY 671 CCAGCAATGGGAGGAGGAGGACGACGATAACAACTCAAGGATGGGAAGATGAT 730
DB 95 lGlnLysTrpAspGlyLysGluThrValIleLysArgLysValValAspGlyAsnLeuLeu 115
QY 731 CGTG 734
DB 115 uVal 116
RESULT 2
Q90W92
```



```

QY 671 CCAGCAATGGGACGAGGAGCAGCAGATACACAGAACTGAAGGATGGAGATGAT 730
Db 95 lGlnLysTrpAspGlyLysGluThrThrLeuValArgGluVal---AspGlyAsnLysLe 114
QY 731 CGTGGTGAGCATC 743
Db 114 uThrLeuThrLeu 118

RESULT 3
Q9XSG4.
ID Q9XSG4 PRELIMINARY; PRT; 113 AA.
AC Q9XSG4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adipocyte lipid-binding protein (Fragment).
GN AP2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=URINARY BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
RT "Expression of ap2 gene in transitional epithelium of rabbit
bladder.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF136241; AAD32209.1; -.
DR HSSP; P04117; 1LJD.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cyFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12536 MW; 4C19A538EC897F4F CRC64;

Alignment Scores:
Pred. No.: 1,51e-11 Length: 113
Score: 179.50 Matches: 51
Percent Similarity: 33.17% Conservative: 16
Best Local Similarity: 25.25% Mismatches: 25
Query Match: 8.02% Indels: 110
DB: Gaps: 1

US-09-788-074-2 (1-1279) x Q9XSG4 (1-113)
QY 131 GGAGTAGGACTGGCTCTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATCAG 190
Db 18 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 37
QY 191 TGTGTATGGCAACATCAGCGTCAAAACCGAGAGCAGCAGTGAAGACGACTGTGTCTCT 250
Db 38 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 57
QY 251 TCTAACTCGGAGAGAGTGTGATGAACGACAGCAGTGTGCGAGAAACAACTCAGGTGACG 310
Db 58 PheLysLeuGlyGlnGluPheAspGluValThrAlaAspArgLysGly-LysSer-- 76
QY 311 TACAACATCTGTGAAGCCAGACAGACTCTTAGATTTCAGATTAAATGGCATTAACAAT 370
Db 76 ----- 76
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 76 ----- 76
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATCAGTTTCTAGATCGAAAA 490
Db 76 ----- 76
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGGTGGAGTTTCAGAGAGGGAAGG 550

```

```

Db 76 ----- 76
QY 551 CGAAGACTTGTGGAGTGTGTGGTCCCTGGGGTTCTTCTTCACTTTGGAAGATGATGAAC 610
Db 76 ----- 76
QY 611 TAACTACCTGTATTTTTCAGACAGGTCTGCACCTTCCAGACGGTGCCTCGTCCAGCA 670
Db 77 -----IleIleThrLeuAspGlyGlyAlaLeuValGlnVa 88
QY 671 CCAGCAATGGGACGAGGAGCAGCAGATACACAGAACTGAAGGATGGAGATGAT 730
Db 88 lGlnLysTrpAspGlyLysSerThrThrIleLysArgLysArgGluGlyAspLysLeuVa 108
QY 731 CGTG 734
Db 108 lVal 109

RESULT 4
O97675
ID O97675 PRELIMINARY; PRT; 99 AA.
AC O97675;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adipocyte fatty acid binding protein (Fragment).
GN AP2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99410873; PubMed=10481259;
RA Ding S.T., McNeel R.L., Mersmann H.J.;
RT "Expression of porcine adipocyte transcripts: tissue distribution and
differentiation in vitro and in vivo.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 123:307-318(1999).
DR EMBL; AF102872; AAC78684.1; -.
DR HSSP; P04117; 1LJD.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cyFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10804 MW; C1E053304FB18F3E CRC64;

Alignment Scores:
Pred. No.: 3.23e-11 Length: 99
Score: 176.50 Matches: 49
Percent Similarity: 33.00% Conservative: 17
Best Local Similarity: 24.50% Mismatches: 24
Query Match: 7.88% Indels: 110
DB: Gaps: 1

US-09-788-074-2 (1-1279) x O97675 (1-99)
QY 137 GGACTGGCTCTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATCAGTGTGAT 196
Db 1 GlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnLeuIleThrValAsn 20
QY 197 GGCAACAACATCAGCTCAAAACCGAGAGCAGTGAAGCAGCAGTGTCTCTTCTTAAC 256
Db 21 GlyAspMetIleThrIleArgSerGluSerThrPheLysAsnThrGluIleAlaPheLys 40
QY 257 CTGGGAGAGAGTGTGATGAACGACAGCTGTGCGAGAAAACTCAGGTACACTACAAC 316
Db 41 LeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValLysSer----- 57
QY 317 ATACTGTGAAGCCAGACAGACTTCTAGATTTCAGATTAAATTCGATTAAACATGTCTGT 376

```

```

Db 57 ----- 57
QY 377 ACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATAAATTAG 436
Db 57 ----- 57
QY 437 TAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAGCACAT 496
Db 57 ----- 57
QY 497 AGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGCGCAAGA 556
Db 57 ----- 57
QY 557 CTTGTTGGAGTGTGTGGTCTCTGGGGTTCCTTTCACCTTTGGAAGATGATGAACATACTA 616
Db 57 ----- 57
QY 617 CCTGTATTTTTCAGACGCTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCACCAAGCA 676
Db 58 -----ThrIleThrLeuAspGlyGlyAlaLeuValGlnValGlnLy 71
QY 677 ATGGGACGGGAAGCAGCAGCATACACAGAAAACCTGAAGGATGGGAAGATGATCGTG 734
Db 71 sTIPAspGlyLysThrThrIleAsnArgLysIleValAspAspLysLeuValVal 90
RESULT 5
Q8QHAB
ID Q8QHAB PRELIMINARY; PRT; 132 AA.
AC Q8QHAB;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Adipocyte fatty acid-binding protein.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Ao J., Wang Q., Meng H., Zhao J., Li J., Wang Y., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid-binding protein gene
in goose.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF479610; AAL79836.1;
SQ SEQUENCE 132 AA; 14772 MW; 5FD4817B02DA31BB CRC64;

Alignment Scores:
Pred. No.: 1.32e-10 Length: 132
Score: 171.50 Matches: 50
Percent Similarity: 33.17% Conservative: 17
Best Local Similarity: 24.75% Mismatches: 25
Query Match: 7.66% Indels: 110
DB: 13 Gaps: 1

US-09-788-074-2 (1-1279) x Q8QHAB (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCAAGCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAACCGAGACACAGACTGTGTCTCTCT 250
Db 45 IleAsnGlyAspValIleThrIleArgSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTGGCGAAGAAAACCTGAGGTCAGC 310
Db 65 PheLysLeuGlyGluGluPheAspGluThrThrAlaAspAspArgLysThr-LysAsn-- 83
QY 311 TACAACATACTGTGAAGCCACAGACAGCTTCTAGATTACAGATTAAATTGCATTACAAAT 370
Db 83 ----- 83

```

```

QY 371 GTCTGTACTTACTGCTCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTTCACCTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACATACCCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 -----ValIleThrLeuAspSerGlyAlaLeuLysGlnVa 95
QY 671 CCAGCAATCGGACGGAAGCAGCAGCATACACAAAACTGAAGATGGGAAGATGAT 730
Db 95 lGlnLysGlyAspGlyLysGluThrValIleLysArgValValValAspGlyAsnLeuLe 115
QY 731 CGTG 734
Db 115 uVal 116
RESULT 6
Q8UWD3
ID Q8UWD3 PRELIMINARY; PRT; 86 AA.
AC Q8UWD3;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Adipocyte fatty acid binding protein (Fragment).
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RA Ao J., Wang Q., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene
in goose.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442493; AAL35352.1;
DR InterPro; IPR000566; Lipoclin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9560 MW; 44789073854EF6C8 CRC64;

Alignment Scores:
Pred. No.: 2.01e-10 Length: 86
Score: 169.50 Matches: 49
Percent Similarity: 33.16% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 21
Query Match: 7.57% Indels: 110
DB: 13 Gaps: 1

US-09-788-074-2 (1-1279) x Q8UWD3 (1-86)
QY 134 GTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCAAGCAGACTGTATCATTCAGTGT 193
Db 1 ValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnValThrIleSerIle 20
QY 194 GATGCCAACAAATCATCGGTCAAACCGAGACACAGTCAAGACGACTGTGTCTCTTGT 253
Db 21 AsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSerPhe 40
QY 254 AACCTGGGAGAGAAGTTTGTGAAACGACAGCTGTGTCGCAAGAAAACACTGAGGTACGTC 313

```

```
Db 41  LysLeuGlyGluPheAspGluThrAlaAspArgLysThr-LysAsn----- 58
QY 314 AACATACTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAAATTCATTAAACAATGTC 373
Db 58 ----- 58
QY 374 TGTACTTACTGCCAAGGGTGAAGTGAACAACTACATTATGGAGTTGACATTTTGATAAAT 433
Db 58 ----- 58
QY 434 TAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTATGAGTTTCTAGATCGAAAGCA 493
Db 58 ----- 58
QY 494 CATAGTTGATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGCGCA 553
Db 58 ----- 58
QY 554 AGACTTGTGGAGTGGTGGGTCTGGGGTTCCTTCACTTTGGAGATGATGAACATA 613
Db 58 ----- 58
QY 614 CTACCCTGTATTTTTCAGACGCTGTCACCTTCCAGAGCGTCCCTGTCAGCACCA 673
Db - 59 -----ValLeuThrLeuGluAsnGlySerLeuLysGlnValG1 71
QY 674 GCAATGGGCGGAGGAGACGACGATAACAAGAAACTGAAGCAT 719
Db 71 nLysTrpAspGlyGluThrLeuLeuLysArgLysValValAsp 86
RESULT 7
Q9DAK4 PRELIMINARY; PRT; 132 AA.
ID Q9DAK4
AC Q9DAK4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 1700008G05RIK protein.
GN 1700008G05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005765; BAB24227.1; -.
DR HSSP; P02690; 1PMP.
DR MGD; MGI:1922747; 1700008G05RIK.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocin_cytFABP.
```

```
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 132 AA; 14758 MW; 7A20C53780845F61 CRC64;
Alignment Scores:
Pred. No.: 2,94e-10 Length: 132
Score: 168.50 Matches: 51
Percent Similarity: 32.84% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 27
Query Match: 7.53% Indels: 110
DB: 11 Gaps: 2
US-09-788-074-2 (1-1279) x Q9DAK4 (1-132)
QY 131 GGATAGGACTGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyArgAlaSerArgLysLeuGlyCysLeuAlaLysProThrValThrIleSer 44
QY 191 TGTGATGGCAACATCAGCGGTCAAAACCGAGAGACAGTGAAGAGGACTGTGTCTCT 250
Db 45 ThrAspGlyAspLeuIleThrIleLysThrLysSerIlePheLysAsnLysGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTGTGATGAAACGACAGCTGATGGCAGAAAACTGAGGTGACG 310
Db 65 PheLysLeuGlyGluPheGluThrProSerGlyArgLysSer-LysSerTh 84
QY 311 TACAACATACTGTGAAGCGACAGAAAGCTTCTAGATTACAGATTAAATTGCATTAACAAT 370
Db 84 r----- 84
QY 371 GTCTGTACTTACTGCCAAGGGTGGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 84 ----- 84
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTTATGATGTTCTAGATCGAAAA 490
Db 84 ----- 84
QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 85 -----ValIleLeu----- 87
QY 551 CGAAGACTGTTGGAGTGGTGGTGGCTGGGGGTTCCTTCACTTTGGAGATGATGAAC 610
Db 87 ----- 87
QY 611 TAACACCTGTATTTTTCAGACAGGTCTGCACCTTCCAAGACGGTCCCTGGTCCAGCA 670
Db 88 -----AspAsnAspSerLeuValGlnVa 95
QY 671 CCAGCAATGGCGGGAAGGAGAGACGACGATACAGAAAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnAspTrpAspGlyLysGluAlaThrIleCysArgLeuValAspGlyLysMetVa 115
QY 731 CGTGGTGAAGC 740
Db 115 lValGluSer 118
RESULT 8
Q9XS15 PRELIMINARY; PRT; 125 AA.
ID Q9XS15
AC Q9XS15;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Heart-type fatty acid-binding protein (Fragment).
GN FABP3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RA Schaap F.G., Pelsers M.M.A.L., van der Vusse G.J., Glatz J.F.C.;
RT "Cloning of equine H-FABP cDNA.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF143950; AAD32219.1; -
DR HSSP: P10790; 1BWY.
DR InterPro: IPR000463; Fatty_acid_BP..
DR InterPro: IPR000586; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
FT NON_TER 1
SQ SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;

Alignment Scores:
Pred. No.: 6.45e-10 Length: 125
Score: 165.50 Matches: 48
Percent Similarity: 32.18% Conservative: 17
Best Local Similarity: 23.76% Mismatches: 27
Query Match: 7.39% Indels: 110
DB: 6 Gaps: 1

US-09-788-074-2 (1-1279) x Q9XS15 (1-125)
QY 131 GGAGTAGGACTGCTCTTAGAGAGATGGTCCATGGCCAGCCAGACTGTATCATACG 190
Db 17 GlyValGlyPheAlaThrArgGlnValAlaAsnMetThrLysProThrThrIleIleGlu 36
QY 191 TGTGATGGCAACAACTACCGGTCAAACCGAGACAGACAGTGAAGACGCTGTCTCT 250
Db 37 ValAsnGlyAspThrIleThrIleLysThrHisSerThrPhelLysAsnThrGluIleSer 56
QY 251 TGTAACTGTCGAGAGAGTTGTATGAACGACAGCTGTGGCAGAAAACTGAGTCAGC 310
Db 57 PhelLysLeuGlyValGluPheAspGluThrThrAlaAspAspArg-LysValLysSer-- 75
QY 311 TACAACATACTGTGAGCGACAGACAGCTTCTAGATTTCACGATTAAATTCATTACAAT 370
Db 75 ----- 75
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAATAACTACTTTATGGAGTTGACTTTTGATA 430
Db 75 ----- 75
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTCTTAGATCGAAAA 490
Db 75 ----- 75
QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGGTGGAGTTCAGAGAGGAAAGG 550
Db 75 ----- 75
QY 551 CGAAGACTTGTGGAGTGGTGGTCCCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 75 ----- 75
QY 611 TAACACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAGAGCGTCCCTGGTCCAGCA 670
Db 76 -----LeuValThrLeuAspGlyGlyLysLeuValHisVa 87
QY 671 CCAGCAATGGGCGGGAAGGAGACGACGATACAAAGAACTCAAGGATGGGAGATGAT 730
Db 87 lGlnGluTrpAsnGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 107
QY 731 CGTG 734
Db 107 eLeu 108

RESULT 9
Q90ZG6 PRELIMINARY; PRT; 111 AA.
AC Q90ZG6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
BT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
```

```
DE D168 protein (Fragment).
GN D168.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
RT "A systematic search for the downstream target genes of the midbrain-
RT MHB reciprocal inductive signaling by ordered differential display
RT revealed the expression of ephrin-A3 in the posterior tectum of
RT zebrafish embryos.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB055675; BAB62806.1; -
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
FT NON_TER 1
SQ SEQUENCE 111 AA; 12444 MW; 82EDA23FDAAB5A8 CRC64;

Alignment Scores:
Pred. No.: 2.37e-09 Length: 111
Score: 160.50 Matches: 47
Percent Similarity: 34.31% Conservative: 23
Best Local Similarity: 23.04% Mismatches: 24
Query Match: 7.17% Indels: 110
DB: 13 Gaps: 3

US-09-788-074-2 (1-1279) x Q90ZG6 (1-111)
QY 125 CCCACAGGAGTAGGACTGGCTCTTAGGAAGATGGTCCATGGCCAGCCAGACTGTATC 184
Db 2 ProLeuGlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrIleVal 21
QY 185 ATTACGTGTGATGGCAACAACTACCGGTCAAACCGAGACAGTGAAGACGACTGTG 244
Db 22 IleSerHisGluGlyAspLysValIleLysThrLeuSerThrPhelLysAsnThrGlu 41
QY 245 TTCTCTTTAACTGGGAGAGAGTTGTATGAACACAGCTGATGGCAAGAACTGAG 304
Db 42 IleSerPhelLysLeuGlyGluGluPheAspGluThrThrAlaAspAspArg-HisVal 61
QY 305 GTCAGCTACAACATACTGTGAGCGGACAGAAAGCTTCTAGATTTCACGATTAAATTCATT 364
Db 61 SSe----- 62
QY 365 AACAAATGTCTGACTTACTTGTGCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTT 424
Db 63 -ThrValSerLeu----- 66
QY 425 TTGCATAAATTAGTAAAGTCCCAGGACTAAGAAATCAAGACATCTTATGAGTTCTAGAT 484
Db 66 ----- 66
QY 485 CGAAAAGCACATAGTTGTATTGTGGAACAAATAATCAGTATGATGGGGTGGAGTTCAGAGAGG 544
Db 66 ----- 66
QY 545 GAAAGCGAAGACTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 604
Db 67 -GluGlyAspAsn----- 70
QY 605 ATGAACTAACTACCTGTTATTTTTCAGAGAGGCTCTGCACCTTCCAAAGACGGTCCCTGGT 664
Db 71 -----LeuVa 72
QY 665 CCAGCACCAAGCAATGGGCGGGAAGGAGAGACGACGATACAAAGAACTCAAGGATGGGAA 724
Db 72 lGlnValGlnArgTrpAspGlyLysGluThrLysPheValArgGluIleLysAspGly 92
QY 725 GATGATCGTG 734
Db 725 -----
```

```
Db 92 smetValMet 95
RESULT 10
Q9H047
ID Q9H047 PRELIMINARY; PRT; 166 AA.
AC Q9H047;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 18.8 kDa protein.
GN DKF2P547J2313.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Koehler K., Beyer A., Mewes H.W., Weill B., Wiemann S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL512688; CAC21646.1; -.
DR HSSP; P10790; LBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
KW Hypothetical protein.
SQ SEQUENCE 166 AA; 18829 MW; 4E88C1139530F07A CRC64;

Alignment Scores:
Pred. No.: 3.44e-09 Length: 166
Score: 159.50 Matches: 50
Percent Similarity: 33.17% Conservative: 18
Best Local Similarity: 24.39% Mismatches: 25
Query Match: 7.12% Indels: 112
DB: 4 Gaps: 4

US-09-788-074-2 (1-1279) x Q9H047 (1-166)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrValIleLeuSer 44
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACAGACAGTGAAGACGACTGTGTCTCT 250
Db 45 GlnGluGlyAspLysValValIleArgThrLeuSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTCGGAGAGAAGTTTGTATGAACGACAGCTGTATGCGCAAGAACTGAGGTCAGC 310
Db 65 PheGlnLeuGlyGluPheAspGluThrThrAlaAspArg 79
QY 311 TACAACATCTGTGGAAGCGACAGAACCTTCTAGATTTACAGATTTAAATGGCATTAACAAT 370
Db 80 -----AsnCys----- 81
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAACTACTTTATGCGAGTTGACTTTTGATA 430
Db 81 ----- 81
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAATA 490
Db 82 -----Lys 82
QY 491 GCACATAGTTGTTATGTAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 83 Ser-ValValSerLeu----- 87
QY 551 CGAAGACTTGTGGAGTGTGGTGGCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 87 ----- 87
QY 611 TAACTACCTGTATTTTTCAGACAGCGTCTGCACCTTTCCAAGACGGT---GCCCTGGTCCA 667

Db 88 -----AspGlyAspLysLeuValIle 94
QY 668 GCACCAGCAATGGGAGCGGAGGAGACGACGATACACAGAACTGAAGATGGGAAGAT 727
Db 94 sileGlnLysTrpAspGlyLysGluThrAsnPheValArgGluIleLysAspGlyLysMe 114
QY 728 GATCGTGGTGAGC 740
Db 114 tValMetValSer 118

RESULT 11
Q9QV90
ID Q9QV90 PRELIMINARY; PRT; 97 AA.
AC Q9QV90;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE LMG-14-FATTY acid-binding protein (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=93191717; PubMed=8447836;
RA Bansal M.P., Medina D.;
RT "Expression of fatty acid-binding proteins in the developing mouse
mammary gland.";
RL Biochem. Biophys. Res. Commun. 191:61-69(1993).
DR HSSP; P10790; LBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR NON_TER 1
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10752 MW; 35CE0EBEEC2004245 CRC64;

Alignment Scores:
Pred. No.: 5.08e-09 Length: 97
Score: 157.50 Matches: 45
Percent Similarity: 32.67% Conservative: 21
Best Local Similarity: 22.28% Mismatches: 26
Query Match: 7.03% Indels: 110
DB: 11 Gaps: 1

US-09-788-074-2 (1-1279) x Q9QV90 (1-97)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 3 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 22
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACAGACAGTGAAGACGACTGTGTCTCT 250
Db 23 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 42
QY 251 TGTAACTCGGAGAGAAGTTTGTATGAACGACAGCTGTATGCGCAAGAACTGAGGTCAGC 310
Db 43 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 61
QY 311 TACAACATCTGTGGAAGCGACAGAACCTTCTAGATTTACAGATTTAAATGGCATTAACAAT 370
Db 61 ----- 61
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAACTACTTTATGCGAGTTGACTTTTGATA 430
Db 61 ----- 61
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAATA 490
Db 61 ----- 61
```

Qy	491	GCACATAGTTGTTATTGTGAACAACAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG	555
Db	61	-----	61
Qy	551	CGAAGACTTGTGGAGTGGTGTGGGTCCCTGGGGGTTCCCTTCACCTTTGGAAGATGATGAAC	610
Db	61	-----	61
Qy	611	TAACACCTGTATTATTTTTCAGACGGTCTGCACCTTCCAAAGAGGGTCCCTGGTCCAGCA	670
Db	62	-----LeuValThrLeuAspGlyGlyLeuIleHisVa	73
Qy	671	CCAGCAATGGGAGGAGGAGCAGCAGTAAACAAGAAAACCTGAAGCATGGGAAGATCAT	730
Db	73	LGlnLysTrpAsnGlyClnGlnLuthrThrLeuThrArgGluArgValAspGlyLysLeuIle	93
Qy	731	CGTG 734	
Db	93	eLeu 94	
RESULT 12			
Q90WI9			
ID	Q90WI9	PRELIMINARY;	PRT; 53 AA.
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)	
DE	Fatty acid binding protein (Fragment).		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
RN	NCBI_TaxID=9031;		
RX	{1}		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SILKY; TISSUE=BLOOD;		
RA	Wang Q., Li N., Deng X.;		
RT	"Cloning and sequencing of fatty acid binding protein gene in		
RT	chicken";		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF332700; AAK50883.1; -.		
DR	InterPro; IPR000566; Lipocln_cytFABP.		
DR	Pfam; PF00061; Lipocalin; 1.		
FT	NON_TER 1		
FT	NON_TER 53		
SQ	SEQUENCE 53 AA; 5681 MW; 3CAC59C5B6EC57FF CRC64;		
Alignment Scores:			
Pred. No.:	8.41e-09	Length:	53
Score:	155.00	Matches:	31
Percent Similarity:	77.36%	Conservative:	10
Best Local Similarity:	58.49%	Mismatches:	12
Query Match:	6.92%	Indels:	0
DB:	13	Gaps:	0
US-09-788-074-2 (1-1279) x Q90WI9 (1-53)			
Qy	131	GGAGTAGACTGGCTCTTAGGAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTCAG	190
Db	1	GlyValGlyPheAlaThrArgLysMetAlaGlyValAlaLysProAsnLeuThrIleSer	20
Qy	191	TGTATGGCAACACATCAGCGGTCAAAACCGGAGAGCACAGTGAAGACGACTGTGTCTCT	250
Db	21	IleAsnGlyAspValIleThrIleArgSerGluSerThrPhelySerThrGluIleSer	40
Qy	251	TGTAACCTGGGAGAGAGTTTGATGAACAGACAGCTCAT	289
Db	41	PhelysLeuGlyGluGluPheAspGluThrThrAlaAsp	53
RESULT 13			
O57665			
ED	O57665	PRELIMINARY;	PRT; 134 AA.
AD	O57665;		

```
QY 668 GCACCAGCAATGGACGGGAAGAGAGACGACGATACACAGAAACCTGAAGGATGGCAAGAT 727
   |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 nlysGlnSerTrpAspGlyLysGluThrAsnIleGluArgGluIleGluAspGlyLysLe 115

QY 728 GATCGTGGTGACATC 743
   |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 uValAlaLysCysIle 120

RESULT 14
Q918N9
ID Q918N9 PRELIMINARY; PRT; 132 AA.
AC Q918N9:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Brain-type fatty-acid binding protein.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Denovan-Wright E.M., Pierce M., Wright J.M.;
RT "Nucleotide sequence of cDNA clones coding for a brain-type fatty acid
RT binding protein and its tissue-specific expression in adult zebrafish
RT (Danio rerio).";
RL Biochim. Biophys. Acta 0:0-0(2000).
DR EMBL; AF237712; AAF79948.1; -.
DR HSSP; PI0790; 1BWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; LipocIn_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 132 AA; 14918 MW; ED59506C71994C55 CRC64;

Alignment Scores:
Pred. No.: 1, 23e-08 Length: 132
Score: 154.50 Matches: 46
Percent Similarity: 34.10% Conservative: 23
Best Local Similarity: 22.77% Mismatches: 23
Query Match: 6.90% Indels: 110
DB: 13 Gaps: 3

US-09-788-074-2 (1-1279) x Q918N9 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCAG 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrIleValIleSer 44

QY 191 TGTGATGGCAACATCATCAGGTGCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45 HisGluGlyAspLysValIleLysThrLeuSerThrPheLysAsnThrGluIleSer 64

QY 251 TGTAACTCGGAGAGAAAGTTTGTATGAACACGACGCTGATGGCAGAAAAACTGAGGTCACC 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 PheLysLeuGlyGluGluPheAspGluThrThrAlaAspAspArg-HisValLysSer-- 83

QY 311 TACAACATCTGTGAAGCGACAGAGACTTCTAGATTTCAGATTAAATTCATTAAACAAT 370
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 -----ThrVa 85

QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 lSerLeu-----87

QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCCAAAA 490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 -----87
```

```
QY 491 GCACATAGTGTATTTGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGGGAAGG 550
   |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 -----GluI 89

QY 551 CGAAGACTTGTGGAGTGGTGTGGTCTCGGGGGTTCCTTTCATTTTGAAGATGATGAAC 610
   |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 yAspAsn-----91

QY 611 TAACTACCCCTGTATTTTTCAGACGCTCTGCACCTTCCAAGACGGTCCCTGGTCCAGCA 670
   |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 -----LeuValGlnVa 95

QY 671 CCAGCAATGGGACGGGAAGGACGACGATACACAGAAAACTGAAGGATGGGAAGATGAT 730
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 lGlnArgTrpAspGlyLysGluThrLysPheValArgGluIleLysAspGlyLysMetVa 115

QY 731 CGTG 734
   |   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 lMet 116

RESULT 15
Q57663
ID Q57663 PRELIMINARY; PRT; 134 AA.
AC Q57663:
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Fatty acid binding protein H6-isoform.
GN H6-FABP.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RT heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92444; AAC60352.1; -.
DR HSSP; PI0790; 1BWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; LipocIn_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15182 MW; D4CBCFD50E131968 CRC64;

Alignment Scores:
Pred. No.: 2, 4e-08 Length: 134
Score: 152.00 Matches: 45
Percent Similarity: 31.07% Conservative: 19
Best Local Similarity: 21.84% Mismatches: 31
Query Match: 6.79% Indels: 111
DB: 13 Gaps: 2

US-09-788-074-2 (1-1279) x Q57663 (1-134)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCAG 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnArgThrLysProAsnLeuValIleSer 44

QY 191 TGTGATGGCAACAAC---ATCACGGTCAAAACCGAGACAGTGAAGACGACTGTGTCTTC 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45 ValAspAspGlnGlyPheValCysLeuLysSerGlnSerThrPheLysThrThrGluIle 64

QY 248 TCTTGTAACTCGGAGAGAAAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTGAGGTC 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 LysPheLysLeuAsnGluProPheGluGluThrThrAlaAspAspArgLysThr-Arg-- 83
```

```
QY 308 AGCTACAACATACTGTGAAGCGACAGACAGCTTCTAGATTTACAGATTAATAATTGCATTAAC 367
Db 83 ----- 83
QY 368 AATGCTCTGTACTTACTGCGCAAGGGTGACTGAAAAAAGTACTTTATGGAGTTGACTTTTG 427
Db 83 ----- 83
QY 428 ATAAATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATCAGTTTCTAGATCGA 487
Db 83 ----- 83
QY 488 AAAGCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAA 547
Db 83 ----- 83
QY 548 AGCGGAAGACTTGTGGAGTGGTGGGTCTCTGGGGTTCCTTCTACTTTGGAAGATGATG 607
Db 83 ----- 83
QY 608 AACTRACTACCCCTGTATTTTTCAGACAGGCTCTGCACCTTCCAAGACGGTGCCCTGGTCCA 667
Db 84 -----ThrValValThrLeuGluAsnGlyLysLeuValG1 95
QY 668 GCACCAGCAATGGCGGAGGAGGACGACGATACACAGAAAAGTCAAGGATGGGAAGAT 727
Db 95 nLysGlnCysTrpaspGlyLysGluThrAsnIleGluArgGluIleGluaspGlyLysLe 115
QY 728 GATCGTGGTGAGCATC 743
Db 115 uValAlaLysCysIle 120
```

Search completed: November 25, 2002, 10:30:58
Job time : 90.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:25:12 : Search time 21 Seconds
(without alignments)
5052.212 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 2239
Sequence: 1 aatggagcaacatgctagc.....tctatgagaaggtgcaatga 1279

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cpn2.1/USPTO.spool/US09788074/runat_25112002_093513_15663/app_query.fasta_1.1415
-DB=SwissProt_40 -QPMF=fastan -SUFFIX=isp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.col -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09788074.ecgn_1.1.27.@runat_25112002_093513_15663 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Match	Length	ID	Description
1	406.5	18.2	135	1 FABLE_MOUSE	Q05816 mus musculus
2	367.5	16.4	135	1 FABLE_RAT	P55053 rattus norv
3	350.5	15.7	135	1 FABLE_HUMAN	Q01469 homo sapien
4	334.5	14.9	135	1 FABLE_BOVIN	P55052 bos taurus
5	200.5	9.0	131	1 MYP2_HABIT	P02691 oryctolagus
6	189.5	8.5	131	1 MYP2_HUMAN	P02689 homo sapien
7	187.5	8.4	131	1 FABA_PIG	Q97788 sus scrofa
8	182.5	8.2	131	1 FABA_SPETR	Q99p60 spermophilu
9	181.5	8.1	132	1 FABL_GINCI	P80049 ginglymosto
10	180.5	8.1	132	1 FABA_BOVIN	P48035 bos taurus
11	177.5	7.9	131	1 MYP2_MOUSE	P24526 mus musculus
12	176.5	7.9	132	1 FABLE_RAT	P07483 rattus norv
13	175.5	7.8	131	1 MYP2_BOVIN	P02690 bos taurus
14	174.5	7.8	131	1 FABA_HUMAN	P15090 homo sapien
15	174	7.8	131	1 FABA_MOUSE	P04117 mus musculus
16	171.5	7.7	132	1 FABL_HUMAN	P05413 homo sapien
17	171.5	7.7	132	1 FABL_SPETR	Q99p51 spermophilu
18	169.5	7.6	132	1 FABL_PIG	O02772 sus scrofa

ALIGNMENTS									
RESULT 1									
ID	FABLE_MOUSE	STANDARD;	PRT;	135	AA.				
AC	Q05816;								
DT	01-FEB-1994 (Rel. 28, Created)								
DT	01-FEB-1994 (Rel. 28, Last sequence update)								
DT	15-JUN-2002 (Rel. 41, Last annotation update)								
DE	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homologue) (PA-FABP) (Keratinocyte lipid-binding protein).								
DE	FABP5 OR MALI OR KLBP OR FABPE.								
GN	Mus musculus (Mouse).								
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Keratinocytes;								
RX	MEDLINE=93352523; PubMed=8349619;								
RA	Krieg P., Feil S., Fuerstenberger G., Bowden T.G.;								
RT	"Tumor-specific overexpression of a novel keratinocyte lipid-binding protein. Identification and characterization of a cloned sequence activated during multistage carcinogenesis in mouse skin.";								
RL	J. Biol. Chem. 268:17362-17369(1993).								
RL	[2]								
RN	SEQUENCE FROM N.A.								
RP	STRAIN=129/SVJ;								
RC	MEDLINE=98332726; PubMed=9666100;								
RX	Bleck B., Hohoff C., Binns B., Kustow B., Dixkens C., Hameister H., Boerchers T., Spener F.;								
RA	"Cloning and chromosomal localisation of the murine epidermal-type fatty acid binding protein gene (fabpe).";								
RL	Gene 215:123-130(1998).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=99013878; PubMed=9795232;								
RA	Hertzel A.V., Bernlohr D.A.;								
RT	"Cloning and chromosomal location of the murine Keratinocyte lipid-binding protein gene.";								
RL	Gene 221:235-243(1998).								
RN	[4]								
RP	SEQUENCE FROM N.A.								

P11404 mus musculus
P82188 lampetra ja
P10790 bos taurus
Q05423 gallus gall
P70623 rattus norv
O15440 homo sapien
Q09139 bos taurus
O13008 oncorhynch
P51880 mus musculus
P55051 rattus norv
Q08716 mus musculus
P55054 rattus norv
P40220 gallus gall
O42386 fugu rubrip
P50568 xenopus lae
P29762 homo sapien
P02695 mus musculus
P29373 homo sapien
Q02970 echinococcu
P29498 schistosoma
P82935 mus musculus
P82980 homo sapien
P09455 homo sapien
Q00315 mus musculus
P02596 rattus norv
Q96705 homo sapien
Q9u5p1 lepidoglyph

RC STRAIN=C57BL/6J; TISSUE=Stomach;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC C18 CHAIN LENGTH (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN KERATINOCTES AND ALSO IN
 CC STRATIFIED EPITHELIA OF EPIDERMIS AND TONGUE. RELATIVELY HIGH
 CC LEVELS FOUND IN ADIPOSE AND MAMMARY TISSUES AND SMALL AMOUNTS
 CC FOUND IN HEART, BRAIN, LIVER, SPLEEN, MUSCLE AND LUNG.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CBPP/CRAFP FAMILY OF
 CC TRANSPORTERS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X70100; CAA49703.1; -;
 DR EMBL; AJ223066; CAA11069.1; -;
 DR EMBL; AF061015; AAC82368.1; -;
 DR EMBL; AF061014; AAC82368.1; JOINED.
 DR EMBL; AK008782; BAB25890.1; -;
 DR EMBL; AK011551; BAB27692.1; -;
 DR EMBL; BC002008; AAH02008.1; -;
 DR PIR; S36635; S36635.
 DR HSSP; Q01469; 1B56.
 DR MGD; MGI:101790; Fapp5.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipoclin_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding.
 SQ SEQUENCE 135 AA; 15137 MW; 6A6C8DBEBB046185 CRC64;
 Alignment Scores:
 Pred. No.: 2 62e-32 Length: 135
 Score: 406.50 Matches: 93
 Percent Similarity: 45.02% Conservative: 2
 Best Local Similarity: 44.08% Mismatches: 6
 Query Match: 18.16% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x FABE_MOUSE (1-135)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTCAG 130
 DB |||||||
 QY 27 GlyValGlyLeuAlaLeuArgLysMetAlaAlaMetAlaLysProAspCysIleIleThr 46
 DB |||||||
 QY 191 TGTGATGGCAACAACATCAGGGTCAAAACCGAGCAGCAGTGAAGACGACTGTGTCTCT 250
 DB |||||||
 QY 47 CysAspGlyAsnAsnIleThrValLysThrGluSerThrValLysThrValPheSer 66
 DB |||||||
 QY 251 TGTAACTCTGGGAGAGAAGTTTGTATGAACGACACAGCTGTGGCGCAAAACCTGAGGTCA 310
 DB |||||||
 QY 67 CysAsnLeuGlyGluLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
 DB |||||||
 QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTACAGATTAATTCATTAACAAT 370
 DB -----
 QY 85 ----- 85
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAANAACACTTTATGGAGTTGACTTTTGATA 430
 DB -----
 QY 85 ----- 85
 QY 431 AATTAGTAAAGTCCCGAGGCTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 DB -----
 QY 85 ----- 85
 QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
 DB -----
 QY 85 ----- 85
 QY 551 CGAAGACTTGTGGAGTGGTGGTCTGGGGTCTTCTTCTTCTTGGAGAGATGATGAAC 610
 DB -----
 QY 85 ----- 85
 QY 611 TAACTACCCTGTATTTTTCAGACGGCTGCACCTTCCAAAGCGGTCCCTGGTCCAGCA 670
 DB |||||||
 QY 86 -----valCysThrPheGlnAspGlyAlaLeuValGlnHI 97
 DB -----
 QY 671 CCAGCAATGGGACGGGAGGAGCAGCAGATAACAAGAACTGAAGATGGGAAGATGAT 730
 DB |||||||
 QY 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetII 117
 QY 731 CGTGGTGACATCAAGACTGGCACCATGC 761
 DB |||||
 QY 117 eValGluCysValMetAsnAlaThrCys 127
 DB |||||
 RESULT 2
 FABE_RAT
 ID FABE_RAT STANDARD; PRT; 135 AA.
 AC P55053; P97757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Fatty acid-binding protein, epidermal (E-FABP) (Cutaneous fatty acid-
 DE binding protein) (C-FABP) (DALI).
 GN FABP5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lens;
 RX MEDLINE=95331629; PubMed=7607553;
 RA Wen Y., Li G.W., Chen P., Wong E., Bekhor I.;
 RT "Lens epithelial cell mRNA. II. Expression of a mRNA encoding a
 RT lipid-binding protein in rat lens epithelial cells.";
 RL Gene 158:269-274(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Skin;
 RX MEDLINE=94220094; PubMed=816694;
 RA Watanabe R., Fujii H., Odani S., Sakakibara J., Yamamoto A., Ito M.,
 RA Ono T.;
 RT "Molecular cloning of a cDNA encoding a novel fatty acid-binding

```

RT protein from rat skin."
RL Biochem. Biophys. Res. Commun. 200:253-259(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-Sprague-Dawley; TISSUE=Nerve;
MEDLINE=96302634; PubMed=8723767;
RA de Leon M., Welcher A.A., Nahin R.H., Liu Y., Ruda M.A.,
Shooter E.M., Molina C.A.;
RT "Fatty acid binding protein is induced in neurons of the dorsal root
ganglia after peripheral nerve injury."
RL J. Neurosci. Res. 44:283-292(1996).
CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
C18 CHAIN LENGTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U13253; AAA86680.1; -
DR EMBL; S69874; AAB30574.1; -
DR EMBL; S83247; AAB46848.1; -
DR HSP; 001469; 1B56.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding.
FT CONFLICT 49 49 G -> N (IN REF. 1).
FT CONFLICT 112 112 K -> N (IN REF. 3).
SQ SEQUENCE 135 AA; 15059 MW; 978392433DF54358 CRC64;

Alignment Scores:
Pred. No.: 135
Score: 367.50 Length: 135
Percent Similarity: 43.13% Matches: 85
Best Local Similarity: 40.28% Conservative: 6
Query Match: 16.41% Mismatches: 10
DB: 1 Indels: 110
1 Gaps: 1

US-09-788-074-2 (1-1279) x FABE_RAT (1-135)
QY 131 GGAGTAGGACTGGCTTATAGGAGATGGCTGCCATGGCCAGCCAGACTGTATCATACG 190
Db 27 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACACATCATCGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
Db 47 LeuAspGlyAsnAsnThrValLysThrGluSerThrValLysThrValPheSer 66
QY 251 TGTAACTCGGAGAGAGTGTGATGAACACGACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 67 CysThrLeuGlyGluLysPheAspGluThrAlaAspGlyArgLysThrGlu-Thr--- 85
QY 311 TACAACATCTCTGTGAAGCGACAGACAGCTTCTAGATTACAGATTAATGTCATTAACAAT 370
Db 85 ----- 85
QY 371 GTCGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 85 ----- 85
QY 431 AATTAGTAAAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 85 ----- 85

```

```

QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 85 ----- 85
QY 551 CGAAGACTGTTGAGTGGTGTGGGTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 85 ----- 85
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTCCCTGTGTCAGCA 670
Db 86 -----ValCysThrPheThrAspGlyAlaLeuValGlnH1 97
QY 671 CCAGCAATGGGACGGGAGGAGGAGGACGATGAACAAAGAACTGAAGATGGGAGATGAT 730
Db 97 sGlnLysTrpGluGlySerThrIleThrArgLysLeuLysAspGlyLysMetVa 117
QY 731 CGTGGTGGAGCTCAAGACGACTGGCACCATGC 761
Db 117 lValGluCysValMetAsnAlaIleCys 127
RESULT 3
FABE_HUMAN
ID FABE_HUMAN STANDARD; PRT; 135 AA.
AC Q01469;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated
DE fatty acid-binding protein homolog) (PA-FABP).
GN FABP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Keratinocytes;
RX MEDLINE=92381332; PubMed=1512466;
RA Madson P.S., Rasmussen H.H., Leffers H., Honore B., Cells J.E.;
RT "Molecular cloning and expression of a novel keratinocyte protein
RT (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is
RT highly up-regulated in psoriatic skin and that shares similarity to
RT fatty acid-binding proteins."
RL J. Invest. Dermatol. 99:299-305(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129.
RX TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
RN [4]
RP SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
RX MEDLINE=94379963; PubMed=8092987;
RA Siegenthaler G., Hotz R., Chatellard-Gruaz D., Didierjean L.,
RA Hellman U., Saurat J.-H.;
RT "Purification and characterization of the human epidermal fatty acid-
RT binding protein: localization during epidermal cell differentiation
RT in vivo and in vitro."
RL Biochem. J. 302:363-371(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=99425110; PubMed=10493790;
RA Hohoff C., Borchers T., Rustow B., Spener F., van Tilbeurgh H.;
RT "Expression, purification and crystal structure determination of
RT recombinant human epidermal-type fatty acid-binding protein."

```

RL Biochemistry 38:12229-12239(1999).
 CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC C18 CHAIN LENGTH. DECREASING THE CHAIN LENGTH OR INTRODUCING
 CC DOUBLE BONDS REDUCES THE AFFINITY. MAY BE INVOLVED IN KERATINOCYTE
 CC DIFFERENTIATION.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: KERATINOCYTES; HIGHLY EXPRESSED IN PSORIATIC
 CC SKIN.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
 CC TRANSPORTERS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M94856; AAA58467.1; -.
 DR EMBL; BC019385; AAH19385.1; -.
 DR PDB; 1B56; 05-OCT-99.
 DR Aarhus/Ghent-2DPAGE; 3007; IEF.
 DR Genew; HGNC:3560; FABP5.
 DR MIM; 605168; -.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding; 3D-structure.
 SQ SEQUENCE 135 AA; 15164 MW; 77D38F8806143D63 CRC64;

Alignment Scores:
 Pred. No.: 9.66e-27 Length: 135
 Score: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FABE_HUMAN (1-135)

QY 131 GGAGTAGGACTGCTCTTAGGAGATGGCTGCCATGCCAAGCAGACTGTATCATTCAG 190
 Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACATCATCAGGTCACAAACCGAGAGCAGTGAAGCAGTGTGTTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAAACACTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGlyLysPheGluGluThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACTGTGAACCGCAGAGAAGCTTCTAGATTACAGATTAAATTGCAATTAACAAT 370
 Db 84 ----- 84
 QY 371 GTCTGTACTTACTGCCAGGGCTGACTGAAACAACTACTTTATGGAGTTCACTTTGAATA 430
 Db 84 ----- 84
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGCAAAA 490
 Db 84 ----- 84
 QY 491 GCACATAGTTGATTGTGAACAAATACGATGATGGGTGCAGTTCAGAGAGGAAAGG 550
 Db 84 ----- 84
 QY 551 CGAAGACTTGTGGAGTGGTGGTGGTCCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610

r.

Db 84 ----- 84
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGCAGTGCCTGTGGTCCAGCA 670
 Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnH1 97
 QY 671 CCAGCAATGGGACGGAGGAGAGCAGCAGTAAACAAGAAACTGAAGATGGGAAGATCAT 730
 Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVal 117
 QY 731 CGTGGTGCAGTCATCAAGCACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127
 RESULT 4
 FABE_BOVIN STANDARD; PRT; 135 AA.
 AC P55052; O62808;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Fatty acid-binding protein, epidermal (E-FABP) (Differentiation-
 DE associated lipid binding protein Lp2).
 GN FABP5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-33 AND 116-129.
 RC TISSUE=Lens;
 RX MEDLINE=97103094; PubMed=8947466;
 RA Jaworski C, Wistow G.;
 RT "LP2, a differentiation-associated lipid-binding protein expressed in
 RT bovine lens.";
 RL Biochem. J. 320:49-54(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Retina;
 RX MEDLINE=98198033; PubMed=9521644;
 RA Kingma P.B., Bok D., Ong D.E.;
 RT "Bovine epidermal fatty acid-binding protein: determination of ligand
 RT specificity and cellular localization in retina and testis.";
 RL Biochemistry 37:3250-3257(1998).
 CC -!- FUNCTION: HIGH SPECIFICITY FOR FATTY ACIDS. HIGHEST AFFINITY FOR
 CC THE UNSATURATED FATTY ACID PALMITATE (C16:0). MAY BE INVOLVED IN
 CC THE UPTAKE AND TRANSPORT OF FATTY ACIDS ESSENTIAL FOR THE
 CC NOURISHMENT OF THE SURROUNDING CELL TYPES. IT IS A POTENTIAL
 CC TARGET FOR OXIDATIVE STRESS DURING CATARACT FORMATION IN LENS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LENS AND RETINA (FOUND IN THE
 CC MUELLER CELLS), MODERATELY ABUNDANT IN HEART AND TESTIS (FOUND IN
 CC THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
 CC TRANSPORTERS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U55188; AAB41297.1; -.
 DR EMBL; AF059507; AAC14711.1; -.
 DR HSSP; Q01469; 1B56.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.

KW Transport; Lipid-binding; Phosphorylation.
FT MOD_RES 22 22 PHOSPHORYLATION (BY TYR-KINASES)
FT CONFLICT 52 L -> P (IN REF. 1).
SQ SEQUENCE 135 AA; 15074 MW; 439B86AF88A34E2A CRC64;

Alignment Scores:
Pred. No.: 3,77e-25 Length: 135
Score: 334.50 Matches: 75
Percent Similarity: 41.71% Conservative: 13
Best Local Similarity: 35.55% Mismatches: 13
Query Match: 14.94% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FABE_BOVIN (1-135)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACGTCTATCATTCAG 190
DB 27 GlyValGlyMetAlaLeuArgLysValGlyAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGACAGTGAAGACGACGTGTCTCTCT 250
DB 47 SerAspGlyLysAsnLeuSerIleIleThrGluSerThrLeuLysThrThrGlnPheSer 66
QY - 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTGAGGTGACG 310
DB 67 CysLysLeuGlyLysPheGluGluThrThrAlaAspGlyArgLysThr-Gln----- 84
QY 311 TACAACATCTGTGAAGCGACAGACAGCTCTAGATTACAGATTAAATTCATTACAAT 370
DB 84 ----- 84
QY 371 GTCTGTACTTACTGCCAAGGGTGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
DB 84 ----- 84
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
DB 84 ----- 84
QY 491 GCACATAGTTGTATTCTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAG 550
DB 84 ----- 84
QY 551 CGAAGACTTGTGGAGTGTGGGCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
DB 84 ----- 84
QY 611 TAACTACCTGTATTTTTCAGACGGCTGTGCACCTTCCAAAGACGGTGCCTGTGTCAGCA 670
DB 85 ----- 97
QY 671 CCAGCAATGGGCGGAAGGAGAGACGACGATACAAAGAAAACTCAAGCATGGGAAGATGAT 730
DB 97 SGInGluTrpAspGlyLysGluSerThrIleThrArgLysLeuGluAspGlyLysLeuVal 117
QY 731 CGTGGTGAGCATCAAAAGCACTGGCCACCATGC 761
DB 117 lValValCysValMetAsnAsnValThrCys 127

RESULT 5
MYP2_RABIT
ID MYP2_RABIT STANDARD; PRT; 131 AA.
AC P02691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

RNA SEQUENCE FROM N.A.
RX MEDLINE=8828063; PubMed=2453513;
RA Narayanan V., Barbosa E., Reed R., Tennekoon G.;
RT "Characterization of a cloned cDNA encoding rabbit myelin P2
protein.";
RL J. Biol. Chem. 263:8332-8337(1988).
RN [2]
RN SEQUENCE OF 1-55.
RX MEDLINE=80094496; PubMed=7356651;
RA Ishaque A., Hofmann T., Rhee S., Eylar E.H.;
RT "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
myelin.";
RL J. Biol. Chem. 255:1058-1063(1980).
RN [3]
RN SEQUENCE OF 55-131.
RX MEDLINE=82098098; PubMed=6172423;
RA Ishaque A., Hofmann T., Eylar E.H.;
RT "The complete amino acid sequence of the rabbit P2 protein.";
RL J. Biol. Chem. 257:592-595(1982).
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CELLS.
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03744; AAA31451.1; -
DR PIR; A03145; MPRB2.
DR PIR; A28081; A28081.
DR HSP; P02690; 1PMP.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000586; Lipocln_cytFABP.
DR Pfam; PF00661; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 72 72 E -> Q (IN REF. 3).
FT CONFLICT 83 83 I -> T (IN REF. 3).
FT CONFLICT 98 98 D -> N (IN REF. 3).
SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;

Alignment Scores:
Pred. No.: 7,87e-12 Length: 131
Score: 200.50 Matches: 55
Percent Similarity: 35.15% Conservative: 16
Best Local Similarity: 27.23% Mismatches: 21
Query Match: 8.95% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MYP2_RABIT (1-131)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACGTCTATCATTCAG 190
DB 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProAsnValIleIleSer 43
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGACAGTGAAGACGACGTGTCTCTCT 250
DB 44 LysLysGlyAspIleIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 63
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTGAGGTGACG 310
DB 117 lValValCysValMetAsnAsnValThrCys 127

Db 64 PheLysLeuGlyGlnGluPheGluThrAlaAspAsnArgLysThr-LysSer-- 82
 QY 311 TACAACATCTGTGAGCGACAGAGCTTCTAGATTTACAGATTAAATGCATTAAACAAT 370
 Db 82 ----- 82
 QY 371 GTCTGTACTTCTCCCAAGGCTGACTGAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTTATGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
 Db 82 ----- 82
 QY 551 CGAAGACTTGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 610
 Db 82 ----- 82
 QY 611 TAACTACCTGTATTTTTCAGAGCGTCTGCACCTTCCAAAGACGGTCCCTGCTCCAGCA 670
 Db 83 ----- 83
 QY 671 CCAGCAATGGACGGAAGGAGCAGCAGTATACAAAGAACTCAAGGATGGGAGGATGAT 730
 Db 94 lGlnLysTrpAspGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 114
 QY 731 CGTG 734
 Db 114 lval 115
 RESULT 6
 ID MYP2_HUMAN STANDARD; PRT: 131 AA.
 AC P02689;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myelin P2 protein.
 GN PMP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92068191; PubMed=1720307;
 RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
 [1]
 RA "Isolation and sequence determination of cDNA encoding P2 protein of
 human peripheral myelin.";
 RT Biochem. Biophys. Res. Commun. 181:204-207(1991).
 RL [2]
 RN SEQUENCE.
 RX MEDLINE=83058785; PubMed=6183401;
 RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;
 RT "The complete amino acid sequence of human P2 protein.";
 RL J. Neurochem. 39:1759-1762(1982).
 RN [3]
 RP SEQUENCE OF 1-115 FROM N.A.
 RX MEDLINE=95054012; PubMed=7525873;
 RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
 RA Tennekoon G.;
 RT "Partial structure and mapping of the human myelin P2 protein gene.";
 RL J. Neurochem. 63:2010-2013(1994).
 CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
 CC CELLS.
 CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
 CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
 CC PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
 CC TRANSPORTERS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: D16181; BAA03726.1;
 DR EMBL: D16179; BAA03726.1; JOINED.
 DR EMBL: D16180; BAA03726.1; JOINED.
 DR EMBL: X62167; CAA44096.1;
 DR EMBL: S73470; AAB32592.2;
 DR EMBL: S73468; AAB32592.2; JOINED.
 DR EMBL: S73469; AAB32592.2; JOINED.
 DR PIR: A03143; MPH02.
 DR PIR: JT0977; JT0977.
 DR HSP: P02690; 1PMP.
 DR Genew: HGNC:9117; PMP2.
 DR MIM: 170715;
 DR InterPro: IPR000463; Fatty_acid_BP.
 DR InterPro: IPR000566; Lipocln_cytFABP.
 DR Pfam: PF00061; lipocalin; 1.
 DR PRINTS: PR00178; FATTYACIDBP.
 DR PROSITE: PS00214; FABP; 1.
 KW Myelin; Lipid-binding; Transport; Acetylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1
 FT DISULFID 117 124
 FT CONFLICT 24 24 G -> GG (IN REF. 3).
 FT CONFLICT 98 98 D -> N (IN REF. 2).
 FT CONFLICT 110 110 N -> D (IN REF. 2).
 SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;

Alignment Scores:

Pred. No.: 9.76e-11 Length: 131
 Score: 189.50 Matches: 53
 Percent Similarity: 34.33% Conservative: 16
 Best Local Similarity: 26.37% Mismatches: 22
 Query Match: 8.46% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MYP2_HUMAN (1-131)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATACG 190
 Db 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleSer 43
 QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGAGCAGCAGTGAAGAGCTGTGTCTCT 250
 Db 44 LysLysGlyAspLeileThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 63
 QY 251 TGTAACTGGGAGAGAAGTTTGATGAACACACAGCTGATGGCAAGAAAGAGGTCAGC 310
 Db 64 PheLysLeuGlyGlnGluPheGluThrAlaAspAsnArgLysThr-LysSer-- 82
 QY 311 TACAACATCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAAATGCATTAAACAAT 370
 Db 82 ----- 82
 QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTTATGTGAACAAATCAGTATGATGGGTGGGTTTCAGAGAGGAAAGG 550

Db 82 ----- 82
QY 551 CGAAGACATTGTTGGAGTGTGTGGTCTGGGGTTCCTTCACTTTGGGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACTACCTGTATTTTGCACACGGTGTGCACCTTCCAGACGGTGGCCCTGGTCCAGCA 670
Db 83 ----- 82
QY 671 CCAGCAATGGGACGGAAGGAGGAGCAGCAATAACAAGAACTGAAGGATGGGAAGATGAT 730
Db 94 IGLnArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 114
QY 731 C 731
Db 114 I 114

RESULT 7
FABA_PIG
ID FABA_PIG STANDARD; PRT; 131 AA.
AC O97788;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding protein) (ALBP) (A-FABP) (AF2).
GN FAP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Dutoc; TISSUE=Liver;
RX MEDLINE=9909248; PubMed=9880671;
RA Gerbens F.N.A., Jansen A., van Erp A.J.M., Harders F.,
RA Meuwissen T.H.E., Kettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;
RT "The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs.";
RL Mamm. Genome 9:1022-1026(1998).
RN [2]
RP SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.
RC TISSUE=Fat;
RX MEDLINE=90241143; PubMed=2334399;
RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
RT "The purification and characterization of a fatty acid binding protein specific to pig (Sus domesticus) adipose tissue.";
RL Biochem. J. 267:373-378(1990).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF INTRAMUSCULAR FAT ACCRETION.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: ADIPOSE TISSUE.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE FAPB/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; Y16039; CAA75995.1; -.
CC EMBL; AJ416020; CAC95166.1; -.
CC HSSP; P04117; 1LID.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocln_cytFABP.
CC Pfam; PF00061; lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA: 14545 MW; 656B0CA08CD4AB2 CRC64;
Alignment Scores:
Pred. No.: 1.54e-10 Length: 131
Score: 187.50 Matches: 52
Percent Similarity: 33.66% Conservative: 17
Best Local Similarity: 25.37% Mismatches: 26
Query Match: 8.37% Indels: 110
DB: 1 Gaps: 1
US-09-788-074-2 (1-1279) x FABA_PIG (1-131)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 24 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnLeuIleThr 43
QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGACGACAGTGAAGACGACTGTGTCTCT 250
Db 44 ValAsnGlyAspMetIleThrIleArgSerGluSerThrPheLysAsnThrGluIleAla 63
QY 251 TGTAACTGGGAGAGAAAGTTTGTGAACACGACAGCTGATGGCAGAAAACTAGAGTCAGC 310
Db 64 PheLysLeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValLysSer-- 82
QY 311 TACAACATCTGTGAAGCCGACAGAACCTCTTAGATTACAGATTAATAATTCATTACAAT 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAANA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTTCTGAACAAAAATCAGTATGATGGGTGGAGTTTCACAGAGCGAAGG 550
Db 82 ----- 82
QY 551 CGAAGACTGTTGGAGTGTGTGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACTACCTGTATTTTTCAGACGCGTCTGCACCTTCCAAGACGGTGGCCCTGGTCCAGCA 670
Db 83 ----- 82
QY 671 CCAGCAATGGGACGGAAGGAGGAGCAGCAGTAAACAAGAACTGAAGGATGGGAAGATGAT 730
Db 94 IGLnLysTrpAspGlyLysThrThrThrIleAsnArgLysIleValAspLysLeuVa 114
QY 731 CGTGGTGGAGCATC 743
Db 114 IValGluCysIle 118
RESULT 8
FABA_SPETR
ID FABA_SPETR STANDARD; PRT; 131 AA.
AC Q99P60;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding protein) (ALBP) (A-FABP).
GN FAP4.
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).

Db	82	-----	82
Qy	551	CGAAGACTTGTTGGAGTGGTGGGTCTTCACTTTTGAAGATGATGAAC	610
Db	82	-----	82
Qy	611	TAACTACCTGTATTMTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTTGGTCCAGCA	670
Db	83	-----	83
Qy	671	CCACCAATGGACGGGAAGACGACGATACACAGAAAACCTCAAGATGGGAGATGAT	730
Db	94	lGlnLysTrpAspGlyLysSerThrThrIleLysArgLysArgLysAspLysLeuVa	114
Qy	731	CGTG 734	
Db	114	lVal 115	
RESULT 9			
FABL_GINCI			
ID	FABL_GINCI	STANDARD;	PRT; 132 AA.
AC	P80049;		
DT	01-MAR-1992 (Rel. 21, Created)		
DT	01-MAR-1992 (Rel. 21, Last sequence update)		
DE	Fatty acid-binding protein, liver (L-FABP).		
OS	Ginglymostoma cirratum (Nurse shark).		
OC	Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;		
OC	Ginglymostomatidae; Ginglymostoma.		
OX	NCBI_TaxID=7801;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Liver;		
RX	MEDLINE=92137215; PubMed=1735421;		
RA	Medzhiradzky K.F., Gibson B.W., Kaur S., Yu Z., Medzhiradzky D.,		
RA	Burlingame A.L., Bass N.M.;		
RT	"The primary structure of fatty-acid-binding protein from nurse shark		
RT	liver. Structural and evolutionary relationship to the mammalian		
RL	fatty-acid-binding protein family";		
RL	Eur. J. Biochem. 203:327-339(1992).		
CC	-i- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR		
CC	TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.		
CC	-i- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-i- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF		
CC	TRANSPORTERS.		
DR	PIR; S20297; S20297.		
DR	HSP; P05413; IHMT.		
DR	InterPro; IPR000463; Fatty_acid_BP.		
DR	InterPro; IPR000586; Lipoclin_cylFABP.		
DR	Pfam; PF00081; Lipocalin; 1.		
DR	PRINTS; PR00178; FATTYACIDBP.		
DR	PROSITE; PS00214; FABP; 1.		
KW	Transport; Lipid-binding; Acetylation; Phosphorylation.		
FT	MOD_RES 1 1		
FT	MOD_RES 19 19		
FT	ACETYLATION		
FT	PHOSPHORYLATION (BY TYR-KINASES)		
FT	(POTENTIAL).		
SQ	SEQUENCE 132 AA; 15079 MW; 2AFDEA2C0BE2095F CRC64;		
Alignment Scores:			
Pred. No.:	6.1e-10	Length:	132
Score:	181.50	Matches:	53
Percent Similarity:	34.33%	Conservative:	16
Best Local Similarity:	26.37%	Mismatches:	22
Query Match:	8.11%	Indels:	110
DB:	1	Gaps:	2
US-09-788-074-2 (1-1279) x FABL_GINCI (1-132)			
Qy	134	GTAGACTGCGCTCTTAGGAAGATGGCTGCATGCCAAGCCAGCTATCATCTGT	193
Db	25	Va1SerLeuAlaGlnArqLysValAlaThrThrValLysProLysThrIleLeuSerLeu	44


```
QY 194 GATGGCAACATCATCGCTCAAAACCGAGACAGACAGTCAAGACGACTGTGTTCTTCT 253
Db 45 AspGlyAspValIleThrLysThrGluSerThrPheLysSerThrAsnIleGlnPhe 64
QY 254 AACCTGGGAGAGAAGTTTCATAAACGACAGCTGTGCGCAGAAACAACTCAGCTCAGCTAC 313
Db 65 LysLeuAlaGluPheAspGluThrThrAlaAspAsnArg ----- 78
QY 314 AACATACCTGTAAGCGACAGAAAGCTTCTAGATTTACAGATTAATTCGATTAAACATGTC 373
Db 78 ----- 78
QY 374 TGTACTTACTGCCAAGGGCTGACTGAAACAACTACTTTATGAGTTGACTTTTGATAAAT 433
Db 79 -----ThrThrLysThrThr----- 83
QY 434 TAGTAAAGTCCAGGACTTAAGAAATGAACATCTTATGAGTTTCTAGATCGAAAAAGCA 493
Db 83 ----- 83
QY 494 CATAGTTGATTGTGAACAAATCATGATGATGGGGTGGAGTTCAGAGAGGAAAGCGA 553
Db 83 ----- 83
QY -554 AGACTTGTGGAGTGGTGGCTCGGGTTCCTTCACTTTGGAGATGATGAACATAA 613
Db 83 ----- 83
QY 614 CTACCCCTGTATTTTTCGACAGCGTCTGTACACCTTCCAAAGAGTGCCTCGTCCAGCACCA 673
Db 84 -----ValLysLeu-GluAsnGlyLysLeuValGlnThrG1 95
QY 674 GCAATGGGAGGAGGAGGAGCAGCAGCAACAAGAACTGAAGGATGGGAAGATGATCGT 733
Db 95 nArgTpaspGlyLysGluThrThrLeuValArgGluLeuGlnAspGlyLysLeuIleLe 115
QY 734 G 734
Db 115 : 115
RESULT 10
FABA_BOVIN
ID FABA_BOVIN STANDARD; PRT; 131 AA.
AC P48035;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
DE FAPB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96355299; PubMed=8702709;
RA Specht B., Bartezko N., Hohoff C., Kuhl H., Franke R.,
RA Boerchers F., Spener F.;
RT "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RL J. Biol. Chem. 271:19943-19949(1996).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC -!- CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FAPB/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```

```
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89244; CAA61532.1; -
DR HSSP; P04117; LLID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF000566; Lipocalin_cytFABP.
DR Pfam; PF000561; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;

Alignment Scores:
Pred. No.: 7.66e-10 Length: 131
Score: 180.50 Matches: 50
Percent Similarity: 32.18% Conservative: 15
Best Local Similarity: 24.75% Mismatches: 27
Query Match: 8.06% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FABA_BOVIN (1-131)
QY 131 GGAGTAGGACTGCCTCTTAGGAAGATGGTCCATGCCAAGCCAGACAGTGTATCATTCAG 190
Db 24 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProThrLeuIleIleSer 43
QY 191 TGTGTGGCAACAATCATCACGGTCAAAACCGAGACAGTGAAGACGACTGTGTTCTCT 250
Db 44 LeuAsnGlyValValThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 63
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTGAGGTCAGC 310
Db 64 PheLysLeuGlyGlnGluPheAspGluIleThrProAspArg-LysValLysSer-- 82
QY 311 TACAACATACTGTGAAGCGACAGCAAGCTTCTAGATTTCACAGATTAATTCACATAAAT 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAAGTACTTTATGGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCAGGACTAAGAATGAAGACATCTTATGAGTTCTAGATCGAAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAAAATCAGTATGATGCGGTGGAGTTCAGAGAGGAAAGG 550
Db 82 ----- 82
QY 551 CGAAGACTGTTGGAGTGGTGGTGGCTGCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACTACCTGTATTTTTCAGACAGGCTGTGCACCTTCCAAAGAGCGTCCCTGTGTCAGCA 670
Db 83 -----IleValAsnLeuAspGluGlyAlaLeuValGlnVa 94
QY 671 CCAGCAATGGGACGGGAAGAGAGACAGTACACAAACAACTCAAGATGGGGAAGATGAT 730
Db 94 lGlnAsnTrpAspGlyLysSerThrThrIleLysArgLysLeuMetAspLysMetVa 114
QY 731 CGTG 734
Db 114 lIeu 115
RESULT 11
```

MYP2_MOUSE
 ID MYP2_MOUSE STANDARD; PRT; 131 AA.
 AC P24526;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myelin P2 protein.
 GN PMP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=91268811; PubMed=1711100;
 RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
 RT "Structure of the mouse myelin P2 protein gene."
 RL J. Neurochem. 57:75-80(1991).
 CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.
 CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL; S39508; AAB19249.2; -
 DR PIR; JH0407; JH0407.
 DR HSP; P02690; LPMP.
 DR MGD; MGI:102667; Pmp2.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR - InterPro; IPR000566; Lipocln_cylFABP.
 DR Pfam; PF00061; Lipocln; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 DR Myelin; Lipid-binding; Transport; Acetylation.
 KW MYELIN; LIPID-BINDING; TRANSPORT; ACETYLATION.
 FT - INIT MET 0 0 BY SIMILARITY.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;
 Alignment Scores:
 Pred. No.: 1.52e-09 Length: 131
 Score: 177.50 Matches: 52
 Percent Similarity: 32.23% Conservative: 16
 Best Local Similarity: 24.64% Mismatches: 33
 Query Match: 7.93% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x MYP2_MOUSE (1-131)
 QY 131 GGAGTAGGACTGCTTTAGGAGATGGCTGCCATGGCCAGCAGCTGTATCATAGC 190
 Db 24 GlyValGlyLeuAlaAsnArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer 43
 QY 191 TGTGATGGCAACAACATACGTCGTCACAAACCCAGAGACACAGTGAAGACGACTGTGTTCTCT 250
 Db 44 LysLysGlyAspPyrIleThrIleArgThrGluSerAlaPheLysAsnThrGluIleSer 63
 QY 251 TGTAACTGGGAGAGTTTGTGAACACAGCAGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAG 310
 Db 64 PheLysLeuGlyGlnGluPheAspGluThrThrAlaAspAsnArgLysAla-LysSer-- 82
 QY 311 TACAACATACTGTGAAGCCAGACAGACCTTCTAGATTACAGATTAAATTCATTACAAAT 370
 Db 82 ----- 82

QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAGTCCAGGAGCTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATCGGGTGGAGTTTCAGAGAGGAAAGG 550
 Db 82 ----- 82
 QY 551 CGAAGACTTGTGGAGCTGCTGGGTCTCTGGGGTCTCTTCACTTTTGAAGATGATGAAC 610
 Db 82 ----- 82
 QY 611 TAACCTACCCTGTATTTTTCAGACGGCTCTGCACCTTCCCAAGAGCGGTCCCTGTCCAGCA 670
 Db 83 -----lleValThrLeuGluArgGlySerLeuLysGlnVa 94
 QY 671 CCAGCAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 730
 Db 94 lGlnLysTrpAspGlyLysGluThrAlaIleArgArgThrLeuLeuAspGlyArgMetVa 114
 QY 731 CGTGTGACATCAAGCACTGGCACCATGC 761
 Db 114 lValGluCysIleMetLysGlyValValCys 124
 RESULT 12
 ID FABH_RAT STANDARD; PRT; 132 AA.
 AC P07483; OQ0Y04;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fatty acid-binding protein, heart (H-FABP).
 GN FABP3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=87250640; PubMed=3036869;
 RA Heukeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
 RT "Analysis of the tissue-specific expression, developmental regulation, and linkage relationships of a rodent gene encoding heart fatty acid binding protein."
 RL J. Biol. Chem. 262:9709-9717(1987).
 RN [2]
 SEQUENCE FROM N.A.
 RX MEDLINE=88107756; PubMed=3427112;
 RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
 RT "Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: identical forms in heart and skeletal muscle."
 RL Biochemistry 26:7900-7904(1987).
 RN [3]
 SEQUENCE.
 RX MEDLINE=88153733; PubMed=3162235;
 RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;
 RT "Revision of the blocked N terminus of rat heart fatty acid-binding protein by liquid secondary ion mass spectrometry."
 RL J. Biol. Chem. 263:4182-4185(1988).
 RN [4]
 PRELIMINARY SEQUENCE.
 RX MEDLINE=86250713; PubMed=2424895;
 RA Sacchettini J.C., Said B., Schulz H., Gordon J.I.;
 RT "Rat heart fatty acid-binding protein is highly homologous to the murine adipocyte 422 protein and the P2 protein of peripheral nerve myelin."
 RL J. Biol. Chem. 261:8218-8223(1986).
 RN [5]

RC SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=91170283; PubMed=2005132;
 RA Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Ono T.;
 RT "Primary structure and cellular distribution of two fatty
 RT acid-binding proteins in adult rat kidneys.";
 RL J. Biol. Chem. 266:5963-5972(1991).
 RN [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Wistar; TISSUE=Heart;
 RX PubMed=10561574;
 RA Zhang J., Rickers-Haunerland J., Dawe I., Haunerland N.H.;
 RT "Structure and chromosomal location of the rat gene encoding the heart
 RT fatty acid-binding protein.";
 RL Eur. J. Biochem. 266:347-351(1999).
 RN [7]
 RN SEQUENCE OF 58-86.
 RX MEDLINE=89374061; PubMed=2775193;
 RA Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
 RT "Rat heart fatty acid-binding protein. Evidence that supports the
 RT amino acid sequence predicted from the cDNA.";
 RL Biochem. J. 260:303-306(1989).
 RN [8]
 RN PARTIAL SEQUENCE.
 RP TISSUE=Stomach;
 RX MEDLINE=90032682; PubMed=2806260;
 RA Kanda T., Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,
 RA Matsubara Y., Muto T., Ono T.;
 RT "Purification and characterization of a fatty-acid-binding protein
 RT from the gastric mucosa of rats. Possible identity with heart
 RT fatty-acid-binding protein and its parietal cell localization.";
 RL Eur. J. Biochem. 185:27-33(1989).
 RN [9]
 RN PARTIAL SEQUENCE.
 RC TISSUE=Mammary gland;
 RX MEDLINE=88326235; PubMed=3415652;
 RA Jones P.D., Carne A., Bass N.M., Grigor M.R.;
 RT "Isolation and characterization of fatty acid binding proteins from
 RT mammary tissue of lactating rats.";
 RL Biochem. J. 251:919-925(1988).
 RN [10]
 RN PARTIAL SEQUENCE.
 RC TISSUE=Mammary gland;
 RX MEDLINE=94162301; PubMed=8117746;
 RA Nielsen S.O., Rump R., Hoerjup P., Roepstorff P., Spener F.;
 RT "Differentiation regulation and phosphorylation of the fatty acid-
 RT binding protein from rat mammary epithelial cells.";
 RL Biochim. Biophys. Acta 1211:189-197(1994).
 CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
 CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,
 CC BRAIN AND MAMMARY GLAND.
 CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CBAP FAMILY OF
 CC TRANSPORTERS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02773; AAA41136.1; -;
 DR EMBL: M18034; AAA41137.1; -;
 DR EMBL: AF144090; AAF19003.1; -;
 DR PIR: A23838; A23838.
 DR PIR: A27452; A27452.
 DR PIR: A28197; A28197.
 DR PIR: A28458; A28458.
 DR PIR: A39551; A39551.
 DR PIR: S06478; S06478.

DR HSP: P05413; LHMT.
 DR InterPro: IPR000463; Fatty_acid_BP.
 DR InterPro: IPR000566; Lipocalin_cytFABP.
 DR Pfam: PF00061; lipocalin; 1.
 DR PRINTS: PR00178; FATTYACIDBP.
 DR PROSITE: PS00214; FABP; 1.
 KW Transport; Lipid-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES).
 FT CONFLICT 63 63 S -> SN (IN REF. 3).
 FT CONFLICT 69 69 E -> Q (IN REF. 5).
 FT CONFLICT 70 70 F -> D (IN REF. 3).
 FT CONFLICT 115 115 L -> LL (IN REF. 6).
 SQ SEQUENCE 132 AA; 14643 MW; 31B4C66A8BF45BE CRC64;
 Alignment Scores:
 Pred. No.: 1.92e-09 Length: 132
 Score: 176.50 Matches: 50
 Percent Similarity: 32.67% Conservative: 16
 Best Local Similarity: 24.75% Mismatches: 26
 Query Match: 7.88% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x FABH_RAT (1-132)
 QY 131 GGAGTAGACTGGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGCTGTATCATACG 190
 Db 24 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 43
 QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 44 LysAsnGlyAspThrIleThrIleYThrHisSerThrPhelYsAsnThrGluIleSer 63
 QY 251 TGTAACTGGGAGAGAGATTTGTGTAACAGCAGCTGTGGCAGAAAACTAGGTCAGC 310
 Db 64 PheGlnLeuGlyValGluPheaspGluValThrAlaaspArg-LysvallySer-- 82
 QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCATTAACAAT 370
 Db 82 ----- 82
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
 Db 82 ----- 82
 QY 431 AATTAGTAAAAAGTCCCGAGGACTAAGAAATAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 82 ----- 82
 QY 491 GCACATAGTTGTATTGTGAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAG 550
 Db 82 ----- 82
 QY 551 CGAAGACTTGTGGAGTGGTGTGGGTCCCTGGGGGTTCCTTCTTGGAGATGATGAAC 610
 Db 82 ----- 82
 QY 611 TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAAGACGGTGCCTGGTCCAGCA 670
 Db 83 -----valValThrLeuAspGlyGlyLysLeuValHisVa 94
 QY 671 CCAGCAATGGGAGGGAAGGAGACGACGATACAAAGAAAACTGAAGGATGGGAAGATGAT 730
 Db 94 GlnLysTrpAspGlyGlnGluThrThrLeuThrArgGluLeuSerAspGlyLysLeuI 114
 QY 731 CGTG 734
 Db 114 eLeu 115
 RESULT 13
 ID MYP2_BOVIN STANDARD: PRT; 131 AA.

AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80225120; PubMed=6156092;
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;
RT "The complete amino acid sequence of the P2 protein in bovine
peripheral nerve myelin.";
RL FEBS Lett. 115:27-30(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=89005045; PubMed=2458918;
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;
RT "The three-dimensional structure of P2 myelin protein.";
RL EMBO J. 7:1597-1604(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=93253782; PubMed=7683727;
RA Cowan S.W., Newcomer M.E., Jones T.A.;
RT "Crystallographic studies on a family of cellular lipophilic
transport proteins. Refinement of P2 myelin protein and the structure
determination and refinement of cellular retinol-binding protein in
complex with all-trans-retinol.";
RL J. Mol. Biol. 230:1225-1246(1993).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CELLS.
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
TRANSPORTERS.
DR PIR; A03144; MPB02.
DR PDB; 1PMP; 26-JAN-95.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
FT MOD_RES 1 124
FT DISULFID 117 124
SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Alignment Scores:
Pred. No.: 2,41e-09 Length: 131
Score: 175.50 Matches: 51
Percent Similarity: 32.67% Conservative: 15
Best Local Similarity: 25.25% Mismatches: 26
Query Match: 7.84% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MYP2_BOVIN (1-131)

QY 131 GGAGTAGGACTGCTTAGGAAGATGGCTGCATGGCCAGCCAGCACTGTATCATTCAG 190
DB 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProArgValIleIleSer 43

QY 191 TGTGATGCCAACATCATCGGTCAAACCCGAGACAGCAGTGAAGACGACTGTGTCTCT 250
DB 44 LysLysGlyAspIleIleThrIleArgThrGluSerProPheLysAsnThrGluIleSer 63

QY 251 TGTAACTGGGAGAGAAAGTTTATGAACACGACAGCTGTATGGCAGAAACACTGAGTCA 310
DB 64 PheLysLeuGlyGlnGluPheGluThrAlaAspAsnArgLysThr-LysSerTh 83

QY 311 TACAACATACTGTGAAGCGACAGCAAGCTTCTAGATTACAGATTAATTTGCATTAACAAT 370
DB 83 rValThrLeuAlaArg----- 88

QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGTATA 430
DB 88 ----- 88

QY 431 AATTAGTAAAGTCCCGAGGACTAAGAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
DB 88 ----- 88

QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
DB 88 ----- 88

QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTCTCTTCACTTTGGAAGATGATGAAC 610
DB 88 ----- 88

QY 611 TAACTACCTCTGTATTTTTCAGACAGGCTCTGCACCTTCCAAAGACGGTGCCTGTGTCACGA 670
DB 89 -----GlySerLeuAsnGlnVa 94

QY 671 CCAGCAATGGGAGGAGACGACGATACACAGAAAACTCAGAGATGGGGAAGATGAT 730
DB 94 LGLnLysTrpAsnGlyAsnGluThrIleLysArgLysLeuValAspLysMetVa 114

QY 731 CGTG 734
DB 114 1Val 115

RESULT 14
FABA_HUMAN
ID FABA_HUMAN STANDARD; PRT; 131 AA.
AC P15090;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
protein) (ALBP) (A-FABP).
GN FABP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90105397; PubMed=2481498;
RA Baxa C.A., Sha R.S., Buelt M.K., Smith A.J., Matarese V.,
RA Chinander L.L., Boundy K.L., Bernlohr D.A.;
RT "Human adipocyte lipid-binding protein: purification of the protein
and cloning of its complementary DNA.";
RL Biochemistry 28:8683-8690(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
TRANSPORTERS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

```
CC EMBL; J02874; AA51689.1; -
DR EMBL; BC003672; AAH03672.1; -
DR PIR; A33363; A33363.
DR HSSP; P04117; 1L1D.
DR Genew; HGNC:3559; FABP4.
DR MIM; 600434; -
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0 BY SIMILARITY.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
FT SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;

Alignment Scores:
Pred. No.: 3,03e-09 Length: 131
Score: 174.50 Matches: 50
Percent Similarity: 32.67% Conservative: 16
Best Local Similarity: 24.75% Mismatches: 26
Query Match: 7.79% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FAB4_HUMAN (1-131)
QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATGCGCCAGCCAGCATGTATCATTCAG 190
Db 24 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 43
QY 191 TGTGTGCGCAACATCATCGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTCT 250
Db 44 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 63
QY 251 TGTAACTCTGGGAGAGAAGTTTGTATGAACAGCAGCTGTGCGCAGAAAACACTGAGTCA 310
Db 64 PheIleLeuGlyGlnGluPheAspGluValThrAlaAspArg-LysValLysSer-- 82
QY 311 TACAACATCTGTGTGAAGCGCAGACAGCTTCTAGATTACAGATTAATAATTCGATTAA 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGTCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTG 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGACAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAATACATATGATGGGTGGAGTTCAGAGAGGGAAG 550
Db 82 ----- 82
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATCAAC 610
Db 82 ----- 82
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGACCTTCCAAAGCGGTGCTGCTCCAGCA 670
Db 83 -----ThrIleThrLeuAspGlyGlyValLeuValHisVa 94
QY 671 CCAGCAATGGGAGGAGAGCAGCAGATACAAAGAACTCAAGATGGGAGATGAT 730
Db 94 lGlnLysPaspGlyLysSerThrThrIleLysArgLysArgGluAspLysLeuVa 114
QY 731 CGTG 734
Db 114 lVal 115
RESULT 15
```

```
FABA_MOUSE
ID FABA_MOUSE STANDARD; PRT; 131 AA.
AC P04117;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (P2 adipocyte protein) (Myelin P2 protein
DE homolog) (3T3-L1 lipid binding protein) (422 protein) (P15).
GN FABP4 OR AP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298159; PubMed=6206497;
RA Bernlohr D.A.; Angus C.W.; Lane M.D.; Bolanowski M.A.; Kelly T.J. Jr.;
RT "Expression of specific mRNAs during adipose differentiation:
RT identification of an mRNA encoding a homologue of myelin P2
RT protein.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233319; PubMed=3520554;
RA Hunt C.R.; Ro J.H.-S.; Dobson D.E.; Min H.Y.; Spiegelman B.M.;
RT "Adipocyte P2 gene: developmental expression and homology of
RT 5'-flanking sequences among fat cell-specific genes.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278164; PubMed=3015943;
RA Phillips M.; Djian P.; Green H.;
RT "The nucleotide sequence of three genes participating in the adipose
RT differentiation of 3T3 cells.";
RN [4]
RP SEQUENCE.
RX MEDLINE=89008309; PubMed=2844775;
RA Matarrese V.; Bernlohr D.A.;
RT "Purification of murine adipocyte lipid-binding protein.
RT Characterization as a fatty acid- and retinoic acid-binding
RT protein.";
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RA Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;
RA Arakawa T.; Hara A.; Fukunishi Y.; Konno H.; Adachi J.; Fukuda S.;
RA Aizawa K.; Izawa M.; Nishi K.; Kiyosawa H.; Kondo S.; Yamanaka I.;
RA Saito T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saito R.;
RA Kadota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Casavant T.;
RA Fleischmann W.; Gaasterland T.; Glissi C.; King B.; Kochiwa H.;
RA Kuehl P.; Lewis S.; Matsuo Y.; Nikola I.; Pesole G.; Quackenbush J.;
RA Schriml L.M.; Staubli F.; Suzuki R.; Tomita M.; Wagner L.; Washio T.;
RA Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.;
RA Blake J.; Boffelli D.; Bojunga N.; Carninci P.; de Bonaldo M.F.;
RA Brownstein M.J.; Bult C.; Fletcher C.; Fujita M.; Gariboldi M.;
RA Gustincich S.; Hill D.; Hofmann M.; Hume D.A.; Kamlya M.; Lee N.H.;
RA Lyons P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombaerts P.;
RA Nordone P.; Ring B.; Ringwald C.; Rodriguez I.; Sakamoto N.;
RA Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibata Y.; Storch K.-F.;
RA Suzuki H.; Toyooka K.; Wang K.H.; Weitz C.; Whittaker C.; Wilming L.;
RA Wynshaw-Boris A.; Yoshida K.; Hasegawa Y.; Kawai H.; Kohsaki S.;
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [6]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=88203618; PubMed=2452440;
RA Cook J.S.; Lucas J.J.; Sibley E.; Bolanowski M.A.; Christy R.J.;
RA Kelly T.J. Jr.; Lane M.D.;
```

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

||||:|||||
Db 94 lGlnLysTrpAspGlyLysSerThrThrIleLysArgLys--ArgAspGlyAspLysIle 113
QY 731 CGTGGTG 737
Db 113 uValVal 115

```

Search completed: November 25, 2002, 10:31:46
Job time : 24 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:25:32 : Search time 42.5 Seconds
(without alignments)
5786.161 Million cell updates/sec

Title: US-09-788-074-2

Perfect score: 2239

Sequence: 1 aatgggagcaacatgctagc.....tctatgagaagtgcataatga 1279

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO_spool/US09788074/runat_25112002_093515_15685/app_query.fasta.1.1415
-DB=PIR_73 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MIN=0 -THR_MAX=100 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09788074.ecgn.1.1_69..runat_25112002_093515_15685 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WMAP -LARGUEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406.5	18.2	135	2 A47497	lipid-binding prot
2	367.5	16.4	135	2 J62201	fatty acid-binding
3	350.5	15.7	135	2 I56326	fatty acid-binding
4	200.5	9.0	132	1 MPRB2	myelin P2 protein
5	189.5	8.5	132	1 MPHU2	myelin P2 protein
6	181.5	8.1	132	2 S20297	fatty acid-binding
7	180.5	8.1	132	2 S57744	adipocyte-type fat
8	177.5	7.9	132	2 JH0407	myelin P2 protein
9	176.5	7.9	133	2 A27452	fatty acid-binding
10	175.5	7.8	131	1 MPBO2	myelin P2 protein
11	174.5	7.8	132	1 F2HUF	fatty acid-binding
12	171.5	7.7	133	1 F2HUC	fatty acid-binding
13	169.5	7.6	132	2 B25952	myelin P2 protein
14	163.5	7.3	133	2 PC4011	fatty acid-binding

15	158.5	7.1	133	2 A34676	fatty acid-binding
16	155.5	6.9	132	2 A49184	fatty acid-binding
17	150.5	6.7	131	2 S06479	fatty acid-binding
18	139.5	6.2	132	2 I58161	lipid-binding prot
19	139.5	6.2	132	2 I48923	fatty acid-binding
20	136.5	6.1	132	2 I56510	fatty acid-binding
21	132.5	5.9	132	2 I52524	testis lipid bindi
22	128.5	5.7	100	2 S13796	retinoic acid-bind
23	126	5.6	136	2 T15207	hypothetical prote
24	123	5.5	95	2 A61629	retinoic acid-bind
25	121	5.4	138	2 I51265	xCRABP - African c
26	120	5.4	137	1 RJHU1	retinoic acid-bind
27	119	5.3	137	1 RJBOA	retinoic acid-bind
28	119	5.3	137	2 A35825	retinoic acid-bind
29	118	5.3	138	1 RJHU2	retinoic acid-bind
30	114	5.1	135	2 T15205	hypothetical prote
31	114	5.1	138	2 A42495	retinoic acid-bind
32	109	4.9	133	2 A39818	14K fatty acid-bin
33	106	4.7	132	2 A48664	fatty acid-binding
34	106	4.7	133	2 A48578	fatty acid-binding
35	106	4.7	134	2 S29600	fatty acid-binding
36	102	4.6	135	1 RJHU0	retinol-binding pr
37	102	4.6	135	1 RJRTO	retinol-binding pr
38	102	4.6	135	2 S16355	retinol-binding pr
39	101	4.3	839	2 T04859	extensin homolog F
40	98.5	4.4	139	2 I53298	cellular retinoic
41	98	4.4	134	2 S69360	retinol-binding pr
42	98	4.4	137	2 T25123	hypothetical prote
43	97.5	4.4	86	2 I50030	cellular retinoic
44	97.5	4.4	134	2 S43470	fatty-acid-binding
45	97.5	4.2	1522	2 T39371	transcription regu

ALIGNMENTS

RESULT 1

A47497 lipid-binding protein, keratinocyte - mouse

N:Alternate names: lipid-binding protein mall

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 13-Aug-1999

C:Accession: A47497; S36635

R:Krieg, P.; Feil, S.; Fuerstenberger, G.; Bowden, G.T.

J. Biol. Chem. 268, 17362-17369, 1993

A:Title: Tumor-specific overexpression of a novel keratinocyte lipid-binding protein.

A:Reference number: A47497; MUID:93352523; PMID:8349619

A:Accession: A47497

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <KRI>

A:Cross-references: EMBL:X70100; PIDN:CAA49703.1; PID:g287986

C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 3.51e-32 Length: 135
Score: 406.50 Matches: 93
Percent Similarity: 45.02% Conservative: 2
Best Local Similarity: 44.08% Mismatches: 6
Query Match: 18.16% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x A47497 (1-135)

QY	131	GGAGTAGGACTGGCTTTAGGAGATGGTGGCCAGCCAGACTGTATCAGG	190
DB	27	GlyValGlyLeuAlaLeuArgLysMetAlaIaMetAlaLysProAspCysIleIleThr	46
QY	191	TGTGTGGCAACACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT	250
DB	47	CysAspGlyAsnIleThrValIysThrGluSerThrValIysThrValPheSer	66
QY	251	TGTAACCTGGGAGAGAAGTTTGTGATGAACACAGCTGTATGGCAGAAAAAAGCTGAGGTCAGC	310

US-09-788-074-2 (1-1279) x JC2201 (1-135)

Qy	131	GGAGTAGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCGACGTGTATCATACG	190
Db	27	GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr	46
Qy	191	TGTGATGGCAACATCATCAGGTCATAAACCGGAGAGCACAGTGAAGACGACTGTGTCTCT	250
Db	47	LeuAspGlyAsnAsnLeuThrValLysThrGluSerThrValLysThrValPheSer	66
Qy	251	TGTAACCTGGGAGAGTGTGATGAACACACAGCTGATGGCAGAAAACTCAGGTCCAGC	310
Db	67	CysThrLeuGlyGluLysPheAspGluThrThrAlaAspGlyArgLysThrGlu---	85
Qy	311	TACAACATACTGTGAAGCGCACAGAAGCTTCTAGATTTACAGATTAAATTTGCATTAAACAAT	370
Db	85	-----	85
Qy	371	GTCGTGACTTACTGCCAAGGGCTGACTGAAAAAACAATCTTTATGGAGTTGACTTTTGATA	430
Db	85	-----	85
Qy	431	AATTAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTTATCAGTTTCTAGATCGAAAA	490
Db	85	-----	85
Qy	491	GCACATAGTTCTATTGTGTGAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG	550
Db	85	-----	85
Qy	551	CGAAGACTTGTTGGAGTGGTGGGTCTGGGCGTTCCTTCACTTTGGAAGATGATGAAC	610
Db	85	-----	85
Qy	611	TAACACCTCTATTTTTGCAGACGGCTGACCTTCCAAGCGGTGCGCTCCAGCA	670
Db	86	-----ValCysThrPheThrAspGlyAlaLeuValGlnIle	97
Qy	671	CCAGCAATGGGCGGGAAGGAGACGACGATGAACAAGAAAACTGAAGGATGGGAAGATGAT	730
Db	97	sGlnLysTrpGluGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetVal	117
Qy	731	CGTGGTGAGCATCAACGCACTGGCACCACATCC	761
Db	117	IValGluCysValMetAsnAsnAlaIleCys	127

RESULT 3
I56326
fatty acid binding protein homolog - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I56326
R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Celis, J.E.
J. Invest. Dermatol. 99, 299-305, 1992
A:Title: Molecular cloning and expression of a novel keratinocyte protein
ilarity to fatty acid-binding proteins.
A:Reference number: I56326; MUID:92381332; PMID:1512466
A:Accession: I56326
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-135 <RES>
A:Cross-references: GB:M94856; NID:gl82353; PIDN:AAA58467.1; PID:gl82354
C:Genetics:
A:Gene: PA-FABP
C:Superfamily: myelin P2 protein

Alignment Scores:		
Pred. No.:	1,44e-26	Length: 135
Score:	350.50	Matches: 78
Percent Similarity:	41.71%	Conservative: 10
Best Local Similarity:	36.97%	Mismatches: 13
Query Match:	15.65%	Indels: 110

DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x I56326 (1-135)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATACG 190
 Db 27 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACATCATCAGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TGTAACTCGGAGAGAAAGTTGATGAACAGCAGCTGATGGCAGAAAACCTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGluLysPheGluThrThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTTCACAGATTAATATGCATTAACAAT 370
 Db 84 ----- 84
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 ----- 84
 QY -431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATCAGTTTCTAGATCGAAAA 490
 Db 84 ----- 84
 QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 84 ----- 84
 QY 551 CGAAGACTTTGTGAGTGTGTGGTCCCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
 Db 84 ----- 84
 QY 611 TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAAGCGGTGCGCTGGTCCAGCA 670
 Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnHi 97
 QY 671 CCAGCAATGGGAGGAGGAGACGATACAAAGAACTCAAGGATGGGAAGATGAT 730
 Db 97 sGlnGluTrpaspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGAGCATCAAGAGCTGGCACCACG 761
 Db 117 lValGluCysValMetAsnValThrCys 127
 RESULT 4
 MPRB2
 myelin P2 protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999
 C:Accession: A28081; A92266; A92372; A03145
 R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.
 J. Biol. Chem. 263, 8332-8337, 1988
 A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.
 A:Reference number: A28081; MUID:88228063; PMID:2453513
 A:Accession: A28081
 A:Molecule type: mRNA
 A:Residues: 1-132 <NAR>
 A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658
 A:Note: translation of initiator Met is not shown
 R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.
 J. Biol. Chem. 255, 1058-1063, 1980
 A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.
 A:Reference number: A92266; MUID:80094496; PMID:7356651
 A:Accession: A92266
 A:Molecule type: protein
 A:Residues: 2-56 <IS1>
 R:Ishaque, A.; Hofmann, T.; Eylar, E.H.
 J. Biol. Chem. 257, 592-595, 1982
 A:Title: The complete amino acid sequence of the rabbit P2 protein.

A:Reference number: A92372; MUID:82098098; PMID:6172423
 A:Accession: A92372
 A:Molecule type: protein
 A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>
 C:Comment: P2 protein and myelin basic protein together constitute a major fraction of
 C:Superfamily: myelin P2 protein
 C:Keywords: acetylated amino end; myelin; phosphoprotein
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:20/Binding site: phosphate (Tyr) (covalent) #status predicted
 F:118-125/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 1-55e-11 Length: 132
 Score: 200.50 Matches: 55
 Percent Similarity: 35.15% Conservative: 16
 Best Local Similarity: 27.23% Mismatches: 21
 Query Match: 8.95% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MPRB2 (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATACG 190
 Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProAsnValIleIleSer 44
 QY 191 TGTGATGGCAACATCATCAGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64
 QY 251 TGTAACTCGGAGAGAAAGTTGATGAACAGCAGCTGATGGCAGAAAACCTGAGGTCAGC 310
 Db 65 PheLysLeuGlyGluPheGluThrThrAlaAspAsnArgLysThr-LysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTTCACAGATTAATATGCATTAACAAT 370
 Db 83 ----- 83
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
 Db 83 ----- 83
 QY 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 83 ----- 83
 QY 551 CGAAGACTTTGTGAGTGTGTGGTCCCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
 Db 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCGACAGCGTCTGCACCTTCCAAAGCGGTGCGCTGGTCCAGCA 670
 Db 84 -----IleIleThrLeuGluArgGlyAlaLeuAsnGlnVa 95
 QY 671 CCAGCAATGGGAGGAGGAGGAGCAGCAGTAAACAAAGAACTCAAGGATGGGAAGATGAT 730
 Db 95 lGlnLysTrpaspGlyLysGluThrThrIleLysArgLysLeuValAspGlyLysMetVa 115
 QY 731 CGTG 734
 Db 115 lVal 116
 RESULT 5
 MPRB2
 myelin P2 protein [validated] - human
 N:Alternate names: peripheral myelin protein 2
 C:Species: Homo sapiens (man)
 C:Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000
 C:Accession: J00977; A03143; S24224
 R:Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human peripheral nerve myelin; JTO977; MUID:92068191; PMID:1720307

A:Accession: JTO977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A:Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785; PMID:6183401

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98, 'N', '100-110', 'D', '112-132' <SUZ>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction of human peripheral nerve myelin

C:Genetics:

A:Gene: GDB:PMP2

A:Cross-references: GDB:129030; OMIM:170715

A:Map position: 8q21.3-8q22.1

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2-132/Product: myelin P2 protein #status experimental <MAT>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.: 1,96e-10 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MPH2 (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTCAG 190

Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleLeuSer 44

QY 191 TGTGATGGCAACATCAGCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCT 250

Db 45 LysLysGlyAspIleThrIleArgThrGluSerThrPhelLysAsnThrGluIleSer 64

QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAAACAGTGAAGTCA 310

Db 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSer-- 83

QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAATAATTGCATTAA 370

Db 83 ----- 83

QY 371 GTCTGTACTTACGCCAAGGCTGACTGAAATAAATACTTTATGGAGTTGACTTTTGATA 430

Db 83 ----- 83

QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490

Db 83 ----- 83

QY 491 GCACATAGTTGTATGTGAACAAATACATGATGGGTGGAGTTCAGAGAGGAAAGG 550

Db 83 ----- 83

QY 551 CGAAGACTTGTGGAGTGTGGTCCCTGGGGTTCCTTCACCTTTGGAAGATGATGAAC 610

Db 83 ----- 83

QY 611 TAACTACCTGTATTTTTCAGACAGGCTGACCTTCCAAAGACGGTGCCTGGTCAGCA 670

Db 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95

QY 671 CCACGAATGGGACGGGAAGGAGACGACGATAAACAAGAAACTGAAGATGGGAAGATGAT 730

Db 95 IGINArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115

QY 731 C 731

Db 115 I 115

RESULT 6

S20297

fatty acid-binding protein, hepatic - nurse shark

C:Species: *Ginglymostoma cirratum* (nurse shark)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Nov-1999

C:Accession: S20297

R:Medzihradsky, K.F.; Gibson, B.W.; Kaur, S.; Yu, Z.; Medzihradsky, D.; Burlingame,

Eur. J. Biochem. 203, 327-339, 1992

A:Title: The primary structure of fatty acid-binding protein from nurse shark liver.

A:Reference number: S20297; MUID:92137215; PMID:1735421

A:Accession: S20297

A:Molecule type: protein

A:Residues: 1-132 <MED>

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; liver; phosphoprotein

F:1/Modified site: acetylated amino end (Val) #status experimental

Alignment Scores:

Pred. No.: 1.24e-09 Length: 132
Score: 181.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.11% Indels: 110
DB: 2 Gaps: 2

US-09-788-074-2 (1-1279) x S20297 (1-132)

QY 134 GTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTCAGT 193

Db 25 ValSerLeuAlaGlnArgLysValAlaThrThrValLysProLysThrIleLeuSerLeu 44

QY 194 GATGGCAACATCAGCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCTTGT 253

Db 45 AspGlyAspValIleThrIleLysThrGluSerThrPhelLysSerThrAsnIleGlnPhe 64

QY 254 AACCTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAAACAGTGAAGTCA 313

Db 65 LysLeuAlaGluGluPheAspGluThrThrAlaAspAsnArg----- 78

QY 314 AACATACCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAATAATTGCATTAA 373

Db 78 ----- 78

QY 374 TGTACTTACGCCAAGGCTGACTGAAATAAATACTTTATGGAGTTGACTTTTGATAAAT 433

Db 79 -----ThrThrLysThrThr----- 83

QY 434 TAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 493

Db 83 ----- 83

QY 494 CATAGTTGTATGTGAACAAATACATGATGGGTGGAGTTCAGAGAGGAAAGCGCA 553

Db 83 ----- 83

QY 554 AGACTTGTGGAGTGTGGTCCCTGGGGTTCCTTCACCTTTGGAAGATGATGAACATA 613

Db 83 ----- 83

QY 614 CTACCTGTATTTTTCAGACAGGCTGCGACCTTCCAAAGACGGTGCCTGGTCAGCACCA 673

Db 84 -----ValLysLeu-GluAsnGlyLysLeuValGlnThrGln 95

QY 674 GCAATGGGACGGGAAGGAGAGCAGCAGTAAACAAGAAACTGAAGGATGGGAAGATGATCGT 733

Db 95 mArgTrpaspGlyLysGluThrThrLeuValArgGluLeuGlnAspGlyLysLeuIleLeu 115
Qy 734 G 734
Db 115 u 115
RESULT 7
S57744
adipocyte-type fatty acid binding protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C:Accession: S57744
R:Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F.
submitted to the EMBL Data Library, June 1995
A:Description: Mammary derived growth inhibitor - not a distinct protein but a mix of he
A:Reference number: S57744
A:Accession: S57744
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <SP>
A:Cross-references: EMBL:X89244; NID:g895753; PIDN:CAA61532.1; PID:g895754
C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 1.56e-09 Length: 132
Score: 180.50 Matches: 50
Percent Similarity: 32.18% Conservative: 15
Best Local Similarity: 24.75% Mismatches: 27
Query Match: 8.06% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x S57744 (1-132)

Qy 131 GGAGTAGGACTGGCTCTTAGGAAGATGGTGCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProThrLeuIleLeuSer 44
Qy 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 45 LeuAsnGlyGlyValValThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 64
Qy 251 TGTAACTGGGAGAGAACTTTCATGAACGACAGCTGATGGCAGAAAACTGAGTCCAGC 310
Db 65 PheLysLeuGlyGlnGluPheAspGluIleThrProAspArg-LysValLysSer-- 83
Qy 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
Qy 371 GTCTGTACTTACTGCCAAGGGTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
Qy 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
Qy 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGGTTCCATGAGAGAGGAAAGG 550
Db 83 ----- 83
Qy 551 CGAAGACTTGTGGAGTGCTGGGTGCTGGGGTTCCTTTCATTTTGAAGATGATGAAC 610
Db 83 ----- 83
Qy 611 TAACTACCTGTATTTTTCACACGGTCTGCACCTTCCAAAGCGGTGCCCTGGTCCAGCA 670
Db 84 -----IleValAsnLeuAspGluGlyAlaLeuValGlnVa 95
Qy 671 CCAGCAATGGGACGGAGGAGACGACGATAACAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 IGlInAsnTrpaspGlyLysSerThrThrIleLysArgLysLeuMetAspLysMetVa 115

Qy 731 CGTG 734
Db 115 ILeu 116

RESULT 8
JH0407

myelin P2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 13-Aug-1999
C:Accession: JH0407
R:Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.
J. Neurochem. 57, 75-80, 1991
A:Title: Structure of the mouse myelin P2 protein gene.
A:Reference number: JH0407; MUID:91268811; PMID:1711100
A:Accession: JH0407
A:Molecule type: DNA
A:Residues: 1-132 <NAR>
A:Cross-references: GB:S39508; NID:g232319; PIDN:AAB19249.1; PID:g232320
C:Comment: This basic protein is found in peripheral and central nervous system myelin
C:Genetics:
A:Introns: 25/1; 82/3; 116/3
C:Superfamily: myelin P2 protein

Alignment Scores:
Pred. No.: 3.13e-09 Length: 132
Score: 177.50 Matches: 52
Percent Similarity: 32.23% Conservative: 16
Best Local Similarity: 24.64% Mismatches: 33
Query Match: 7.93% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x JH0407 (1-132)

Qy 131 GGAGTAGGACTGGCTCTTAGGAAGATGGTGCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyLeuAlaAsnArgLysLeuGlyAsnLeuAlaLysProThrValIleLeuSer 44
Qy 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysLysGlyAspTyrIleThrIleArgThrGluSerAlaPheLysAsnThrGluIleSer 64
Qy 251 TGTAACTGGGAGAGAACTTTCATGAACGACAGCTGATGGCAGAAAACTGAGTCCAGC 310
Db 65 PheLysLeuGlyGlnGluPheAspGluThrThrAlaAspAsnArgLysAla-LysSer-- 83
Qy 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
Qy 371 GTCTGTACTTACTGCCAAGGGTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
Qy 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
Qy 491 GCACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGGTTCCATGAGAGAGGAAAGG 550
Db 83 ----- 83
Qy 551 CGAAGACTTGTGGAGTGCTGGGTGCTGGGGTTCCTTTCATTTTGAAGATGATGAAC 610
Db 83 ----- 83
Qy 611 TAACTACCTGTATTTTTCACACGGTCTGCACCTTCCAAAGCGGTGCCCTGGTCCAGCA 670
Db 84 -----IleValThrLeuGluArgGlySerLeuLysGlnVa 95
Qy 671 CCAGCAATGGGACGGAGGAGACGACGATAACAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 IGlInLysTrpaspGlyLysGluThrAlaIleArgArgThrLeuLeuAspGlyArgMetVa 115

QY 731 CGTGGTGAGCATCAACCACTGGCACCATGC 761
 Db 115 lValGluCysIleMetLysGlyValValCys 125
 RESULT 9
 A27452
 fatty acid-binding protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 13-Aug-1999
 C:Accession: A28458; A27452; A39551; A28197; S06478; S02471
 R:Heuckeroth, R.O.; Birkemeier, E.H.; Levin, M.S.; Gordon, J.I.
 J. Biol. Chem. 262, 9709-9717, 1987
 A:Title: Analysis of the tissue-specific expression, developmental regulation, and linkage of the rat fatty acid-binding protein gene.
 A:Reference number: A28458; MUID:87250640; PMID:3036869
 A:Accession: A28458
 A:Molecule type: mRNA
 A:Residues: 1-133 <HEU>
 A:Cross-references: GB:J02773; NID:g204077; PIDN:AAA41136.1; PID:g204078
 R:Clafrey, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.
 Biochemistry 26, 7900-7904, 1987
 A:Title: Cloning and tissue distribution of rat heart fatty acid binding protein mRNA.
 A:Reference number: A27452; MUID:88107756; PMID:3427112
 A:Accession: A27452
 A:Molecule type: mRNA
 A:Residues: 1-133 <CLA>
 A:Cross-references: GB:M18034; NID:g204079; PIDN:AAA41137.1; PID:g204080
 R:Sacchettini, J.C.; Said, B.; Schulz, H.; Gordon, J.I.
 J. Biol. Chem. 261, 8218-8223, 1986
 A:Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocyte protein.
 A:Reference number: A23838; MUID:86250713; PMID:2424895
 A:Accession: A23838
 A:Molecule type: protein
 A:Residues: 'TEKN', 5-50, 'YG', 53-64, 'N', 65-70, 'D', 72-133 <SAC>
 A:Experimental source: heart
 R:Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.
 J. Biol. Chem. 266, 5963-5972, 1991
 A:Title: Primary structure and cellular distribution of two fatty acid-binding proteins from rat heart.
 A:Reference number: A39551; MUID:91170283; PMID:2005132
 A:Accession: A39551
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 10-69, 'Q', 71-121, 'D', 123-133 <KIM>
 A:Experimental source: kidney
 R:Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.
 J. Biol. Chem. 263, 4182-4185, 1988
 A:Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by 10-69.
 A:Reference number: A28197; MUID:88153733; PMID:3162235
 A:Accession: A28197
 A:Molecule type: protein
 A:Residues: 2-10; 46-53 <GTB>
 R:Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.; Murakami, J.
 Eur. J. Biochem. 185, 27-33, 1989
 A:Title: Purification and characterization of a fatty-acid-binding protein from the gastrophilus.
 A:Reference number: S06478; MUID:90032682; PMID:2806260
 A:Accession: S06478
 A:Molecule type: protein
 A:Residues: 1-133 <KAN>
 A:Experimental source: stomach
 R:Jones, P.D.; Carne, A.; Bass, N.M.; Grigor, M.R.
 Biochem. J. 251, 919-925, 1988
 A:Title: Isolation and characterization of fatty acid binding proteins from mammary tissue.
 A:Reference number: S02471; MUID:88326235; PMID:3415652
 A:Accession: S02471
 A:Molecule type: protein
 A:Residues: 16-22; 32-45; 54-59, 'XX', 62-63, 'X', 65-70; 83-93; 97-107; 117-127 <JOM>
 A:Experimental source: strain Wistar; mammary
 C:Superfamily: myelin p2 protein
 C:Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
 F:1-133/Product: fatty acid-binding protein #status experimental <MAT>

F:1/Modified site: acetylated amino end (Met) #status predicted

Alignment Scores:
 Pred. No.: 3 94e-09 Length: 133
 Score: 176.50 Matches: 50
 Percent Similarity: 32.67% Conservative: 16
 Best Local Similarity: 24.75% Mismatches: 26
 Query Match: 7.88% Indels: 110
 DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x A27452 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCAGACAGCTGTATCATTCAG 190
 Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
 QY 191 TGTGATGGGCAACATCATCGGTCAAACCGAGACAGCTGAAGACGAGCTGTCTCT 250
 Db 45 LysAsnGlyAspThrIleThrIleLysThrHisSerThrPheLysAsnThrGluIleSer 64
 QY 251 TGTAACTCTGGGAGAGTGTGATGAACGACAGCTGCATGCAGAAACAGTGGTCTCAG 310
 Db 65 PheGlnLeuGlyValGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAAATGCATTAACAAT 370
 Db 83 ----- 83
 QY 371 GTCTGTACTTACGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
 Db 83 ----- 83
 QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAACACATCTTATGAGTTCTAGATCGAAAA 490
 Db 83 ----- 83
 QY 491 GCACATAGTTGATTGTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
 Db 83 ----- 83
 QY 551 CGAAGACTTGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 610
 Db 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGAGCGTCTGCACCTTCCAGAGCGTCCCTGCTCCAGCA 670
 Db 84 -----ValValThrLeuAspGlyGlyLeuValHisVa 95
 QY 671 CCAGCAATGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
 Db 95 LGLysTrpAspGlyGlnGluThrThrLeuThrArgGluLeuSerAspGlyLysLeuI 115
 QY 731 CGTG 734
 Db 115 eLeu 116
 RESULT 10
 MBP02
 myelin P2 protein - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 05-Aug-1994
 C:Accession: A03144
 R:Kitamura, K.; Suzuki, M.; Suzuki, A.; Uyemura, K.
 FEBS Lett. 115, 27-30, 1980
 A:Title: The complete amino acid sequence of the P2 protein in bovine peripheral nerve.
 A:Reference number: A03144; MUID:80225120; PMID:6156092
 A:Accession: A03144
 A:Molecule type: protein
 A:Residues: 1-131 <KIT>
 C:Superfamily: myelin p2 protein
 C:Keywords: acetylated amino end
 F:1/Modified site: acetylated amino end (Ser) #status experimental
 F:117-124/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.: 4,96e-09 Length: 131
Score: 175.50 Matches: 51
Percent Similarity: 32.67% Conservative: 15
Best Local Similarity: 25.25% Mismatches: 26
Query Match: 7.84% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x MPB02 (1-131)

QY 131 GGAGTAGGACTGGCTCTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATTTACG 190
Db 24 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProArgValIleIleSer 43
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 44 LysLysGlyAspIleIleThrIleArgThrGluSerProPheLysAsnThrGluIleSer 63
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTGGCAGAAAACTAGAGTCAGC 310
Db 64 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSerTh 83
QY 311 TACAACATCTGTGAAGCCGACAGAACTTCTAGATTACAGATTAAATTCATTAACAAT 370
Db 83 rValThrLeuAlaArg----- 88
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 88 ----- 88
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 88 ----- 88
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGGGAAAGG 550
Db 88 ----- 88
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTTCCCTTCAAGACGGTCCCTTCAAGAGATGATGAAC 610
Db 88 ----- 88
QY 611 TAACTACCTGTATTTTGCAGACGCTCTGCACCTTCCAAAGCGGTCCCTTCCAGCA 670
Db 89 -----GlySerLeuAsnGlnVa 94
QY 671 CCAGCAATGGGACGGAGGAGACGACGATACAAACAACTGAAGATGGGAAGATGAT 730
Db 94 LGlnLysTrpAsnGlyAsnGluThrThrIleLysArgLysLeuValAspGlyLysMetVa 114
QY 731 CGTG 734
Db 114 lVal 115

RESULT 11

FZHUF
fatty acid-binding protein, adipocyte - human
N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein 4
C:Species: Homo sapiens (man)
C:Date: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C:Accession: A33363
R:Baxa, C.A.; Sha, R.S.; Buel, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Boundy
Biochemistry 28, 8683-8690, 1989
A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloning
A:Reference number: A33363; MUID:90105397; PMID:2481498
A:Accession: A33363
A:Molecule type: mRNA
A:Residues: 1-132 <BAX>
A:Cross-references: GB:J02874; NID:q178346; PIDN:AAA51689.1; PID:q178347
A:Experimental source: subcutaneous fat
A:Genetics:
A:Gene: GDB:FABP4

A:Cross-references: GDB:128030

A:Map position: lp33-lp32
C:Superfamily: myelin P2 protein
C:Keywords: blocked amino end; lipid binding; phosphoprotein
F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #st
F:20/Binding site: phosphate (Tyr) (covalent) #status predicted
F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Alignment Scores:

Pred. No.: 6,25e-09 Length: 132
Score: 174.50 Matches: 50
Percent Similarity: 32.67% Conservative: 16
Best Local Similarity: 24.75% Mismatches: 26
Query Match: 7.79% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x FZHUF (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATTTACG 190
Db 25 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTGGCAGAAAACTAGAGTCAGC 310
Db 65 PheIleLeuGlyGlnGluPheAspGluValThrAlaAspAspArg-LysValLysSer-- 83
QY 311 TACAACATCTGTGAAGCCGACAGAACTTCTAGATTACAGATTAAATTCATTAAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTCACITTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTTCCCTTCAAGACGGTCCCTTCAAGAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGCTCTGCACCTTCCAAAGCGGTCCCTTCCAGCA 670
Db 84 -----ThrIleThrLeuAspGlyGlyValLeuValHisVa 95
QY 671 CCAGCAATGGGACGGAGGAGACGACGATACAAACAACTGAAGATGGGAAGATGAT 730
Db 95 LGlnLysTrpAspGlyLysSerThrThrIleLysArgLysGluAspGlyLysLeuVa 115
QY 731 CGTG 734
Db 115 lVal 116

RESULT 12

FZHUF
fatty acid-binding protein, cardiac and skeletal muscle - human
N:Alternate names: fatty acid-binding protein 3 (FABP3)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1991 #sequence_revision 03-May-1996 #text_change 16-Jul-1999
C:Accession: S15432; JH0199; S00603; I54275; A27248
R:Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.
Biochem. J. 276, 203-207, 1991
A:Title: Cloning of the cDNA encoding human skeletal muscle fatty-acid-binding protei
A:Reference number: S15432; MUID:91248148; PMID:1710107

A:Residues: 2-110,'G',112-132 <MAT>
R:Cook, K.S.; Hunt, C.R.; Spiegeleman, B.M.
J. Cell Biol. 100, 514-520, 1985
A:Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcriptional
A:Reference number: 149440; MUID:85105214; PMID:3968175
A:Accession: 149440
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 11-110,'G',112-132 <RES>
A:Cross-references: GB:M28726; NID:g191492; PIDN:AAA37112.1; PID:g191493
R:Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.; Lan
Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988
A:Title: Expression of the differentiation-induced gene for fatty acid-binding protein 1
A:Reference number: 149467; MUID:86203618; PMID:2452440
A:Accession: 149467
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RE2>
A:Cross-references: GB:M20497; NID:g191743; PIDN:AAA37188.1; PID:g191744
A:Experimental source: 3T3-L1 cells
C:Genetics:
C:Superfamily: myelin P2 protein
C:Keywords: lipid binding; phosphoprotein
Alignment Scores:
Pred. No.: 1.98e-08 Length: 132
Score: 169.50 Matches: 49
Percent Similarity: 32.67% Conservative: 17
Best Local Similarity: 24.26% Mismatches: 26
Query Match: 7.57% Indels: 110
DB: 2 Gaps: 1
US-09-788-074-2 (1-1279) x B25952 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 44
QY 191 TGTGTGTCGAACACATCACGGTCAAAACCGAGACGACAGTGAAGCAGCAGCTGTGTCTCT 250
Db 45 ValAsnGlyAspLeuValThrIleArgSerGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAAGTTGATGAACACGACAGCTGATGGCAGAAAACTGAGTCCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluIleThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATCTCTGAAGCGACAGAACTCTAGATTACAGATTAAATGCAATTACCAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGAGCTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 CCACATAGTTGTATTGTGAACAAATCAGTATGATGTTGGGTGGAGTTTCAGAGGGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTTGTGAGTGGTGTGGTCTCTGGGGTTCCTTTCACCTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCCCTGTATTTTTCAGACGCTGTCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 -----IleIleThrLeuAspGlyGlyAlaLeuValGlnVa 95
QY 671 CCAGCAATGGGACGGAGAGACGACCATACACAGAAAACTGAAGGATGGGAAGATGAT 730
Db 83 ----- 83

Db 95 IGLNlystrpaspGlyLysSerThrThrIleLysArgLysArgspValAspLysLeuVa 115
QY 731 COTG 734
Db 115 lVal 116
RESULT 14
PC4011
fatty acid-binding protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jun-1995 sequence revision 14-Jul-1995 #text_change 13-Aug-1999
C:Accession: PC4011; S04591; S05278; PC1248
R:Freuner, M.; Kozak, C.A.; Gallahan, D.; Grosse, R.; Mueller, T.
Gene 147, 237-242, 1994
A:Title: Cloning and characterization of the mouse gene encoding mammary-derived grow
A:Reference number: PC4011; MUID:95011621; PMID:7926807
A:Accession: PC4011
A:Molecule type: mRNA
A:Residues: 1-133 <TR>
A:Cross-references: GB:U02884; NID:g409956; PIDN:AAA61933.1; PID:g409957
R:Tweedie, S.; Edwards, Y.
Nucleic Acids Res. 17, 4374, 1989
A:Title: cDNA sequence for mouse heart fatty acid binding protein, H-FABP.
A:Reference number: S04591; MUID:89296486; PMID:2740224
A:Accession: S04591
A:Molecule type: mRNA
A:Residues: 1-33,'G',35-98,'D',100-133 <TWE>
A:Cross-references: EMBL:X14961; NID:g51266; PIDN:CAA33084.1; PID:g51267
R:Tweedie, S.; Edwards, Y.
submitted to the EMBL Data Library, April 1989
A:Reference number: S05278
A:Accession: S05278
A:Molecule type: mRNA
A:Residues: 1-2,'ER',5-33,'G',35-98,'D',100-133 <TW2>
A:Cross-references: EMBL:X14961
A:Experimental source: cardiac
R:Bansal, M.P.; Medina, D.
Biochem. Biophys. Res. Commun. 191, 61-69, 1993
A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gl
A:Reference number: PC1248; MUID:93191717; PMID:8447836
A:Accession: PC1248
A:Molecule type: protein
A:Residues: 23-108,'R',110-119 <BAN>
A:Experimental source: mammary gland
C:Comment: This protein functions as an endogenous growth inhibitor and differentiat
C:Genetics:
A:Gene: mdgi/h-fabp
A:Introns: 24/1; 82/2; 133/1
C:Superfamily: myelin P2 protein
C:Keywords: lipid binding
Alignment Scores:
Pred. No.: 7.91e-08 Length: 133
Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 2 Gaps: 1
US-09-788-074-2 (1-1279) x PC4011 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGTGTCGAACACATCACGGTCAAAACCGAGACGACAGTGAAGCAGCAGCTGTGTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
QY 251 TGTAACTGGGAGAGAACTTTCATGAACGACAGCTGATGGCAGAAAACTGAGGTCCAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83

QY 311 TACAACATACTGTGAAGCGCAGAGAAGCTTCTAGATTACAGATTAAATTGCATTAAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAGGGCTGACTGAAAACTACTTTATGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAACTCCAGGACTAAGAAATGAACACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTTTCTCAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGCTCTGGGGGTTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 -----LeuValThrLeuAspGlyGlyLysLeuIleHisVa 95
QY 671 CCAGCAATGGGAGGAGGAGCAGCAATACAAAGAACTGAAGGATGGAAGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrThrLeuThrArgGluLeuValAspGlyLysLeuI 115
QY 731 CGTG 734
Db 115 eLeu 116
RESULT 15
A34676
fatty acid-binding protein, cardiac - bovine
N:Alternate names: mammary-derived growth inhibitor
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 13-Aug-1999
C:Accession: A34676; S01133; A37883; A29466
R:Kurtz, A.; Vogel, F.; Funke, K.; Heldin, C.H.; Grosse, R.
J. Cell Biol. 110, 1779-1789, 1990
A:Title: Developmental regulation of mammary-derived growth inhibitor expression in bovi
A:Reference number: A34676; MUID:90243786; PMID:2335570
A:Accession: A34676
A:Molecule type: mRNA
A:Residues: 1-133 <CUR>
A:Cross-references: GB:X51933; NID:g526; PIDN:CAA36199.1; PID:g527
A:Experimental source: mammary gland
R:Billlich, S.; Wissel, T.; Kratzin, H.; Hahn, U.; Hagenhoff, B.; Lezius, A.G.; Spener, F
Eur. J. Biochem. 175, 549-556, 1988
A:Title: Cloning of a full-length complementary DNA for fatty-acid-binding protein from
A:Reference number: S01133; MUID:88315634; PMID:3409882
A:Accession: S01133
A:Molecule type: mRNA
A:Residues: 1-133 <BIL>
A:Cross-references: EMBL:X12710; NID:g338; PIDN:CAA31212.1; PID:g339
A:Experimental source: heart
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:Unterberg, C.; Boerchers, T.; Hojrup, P.; Roepstorff, P.; Knudsen, J.; Spener, F.
J. Biol. Chem. 265, 16255-16261, 1990
A:Title: Cardiac fatty acid-binding proteins. Isolation and characterization of the mito
A:Reference number: A37883; MUID:90375486; PMID:2398054
A:Accession: A37883
A:Molecule type: protein
A:Residues: 2-133 <UNT>
A:Experimental source: heart
A:Note: 99-Asp was also found
R:Boehmer, F.D.; Kraft, R.; Otto, A.; Wernstedt, C.; Hellman, U.; Kurtz, A.; Mueller, T.
J. Biol. Chem. 262, 15137-15143, 1987
A:Title: Identification of a polypeptide growth inhibitor from bovine mammary gland. Seq
A:Reference number: A29466; MUID:86033096; PMID:3667628
A:Accession: A29466
A:Molecule type: protein

A:Residues: 2-12,'S',14,'E',16-40,'L',42-43,'S',45-93,'Q',95-127,'V',129-132 <BOE>
A:Experimental source: mammary gland
A:Note: 13-Asp, 15-Lys, 94-His and 128-Thr were also found
C:Superfamily: myelin P2 protein
C:Keywords: acetylated amino end; cardiac muscle; heart; phosphoprotein
F:2-133/Product: fatty acid-binding protein, cardiac #status experimental <MAT>
F:2/Modified site: acetylated amino end (Val) (in mature form) #status experimental

Alignment Scores:
Pred. No.: 2 51e-07 Length: 133
Score: 158.50 Matches: 45
Percent Similarity: 31.28% Conservative: 21
Best Local Similarity: 21.33% Mismatches: 35
Query Match: 7.08% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x A34676 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGCAACAACATCAGGCTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
Db 45 ValAsnGlyAspThrValIleIleLysThrGlnSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTCATGAAACGACAGCTGATGGCAGAAAACTCAGGTCCAG 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGCAGAGAAGCTTCTAGATTACAGATTAAATTGCATTAAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTTTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGCTCTGGGGGTTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 -----IleValThrLeuAspGlyGlyLysLeuIleHisVa 95
QY 671 CCAGCAATGGGAGGAGGAGCAGCAATACAAAGAACTGAAGGATGGAAGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrSerLeuValArgGluMetValAspGlyLysLeuI 115
QY 731 CGTGTGAGCATCAAGGACTGGCCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

Search completed: November 25, 2002, 10:33:19
Job time : 45.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:28:03 ; Search time 11.5 Seconds
(without alignments)
3483.661 Million cell updates

Title: US-09-788-074-2

Perfect score:

Sequence: 1 aatqqqaqcaacatgctaqc.....tctatqqaqaqqatqcaatqa 1279

Scoring table: BLOSUM62

Xgapop	10.0	,	Xgapext	0.5
Ygapop	10.0	,	Ygapext	0.5
Fgapop	6.0	,	Fgapext	7.0
Delop	6.0	,	Delext	7.0

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 200960

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

```

Command line parameters:
-MODE=frames-nzp.model -DEV=xlp
-O/cgcn2/USPTO.spool/US09788074/runat_25112002_093516_15728/app_query.fasta_1.1415
-Da-published-Applications_AA -OFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blasmus0.1
-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09788074 -CGCN_1_1_10 -runat_25112002_093516_15728
-NCPU=6 -ICPU=3 -NO_XLPX -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIME=30 -THREADS=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -XGAPO=10 -XGAPEXT=0.5 -FCAPOP=6
-DEFLX=7

```

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/us08_NEW_PUB.psp: *
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.psp: *
- 3: /cgn2_6/ptodata/2/pubpaa/us06_NEW_PUB.psp: *
- 4: /cgn2_6/ptodata/2/pubpaa/us06_PUBCOMB.psp: *
- 5: /cgn2_6/ptodata/2/pubpaa/us07_NEW_PUB.psp: *
- 6: /cgn2_6/ptodata/2/pubpaa/us07_PUBCOMB.psp: *
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.psp: *
- 8: /cgn2_6/ptodata/2/pubpaa/us08_PUBCOMB.psp: *
- 9: /cgn2_6/ptodata/2/pubpaa/us09_NEW_PUB.psp: *
- 10: /cgn2_6/ptodata/2/pubpaa/us09_PUBCOMB.psp: *
- 11: /cgn2_6/ptodata/2/pubpaa/us10_NEW_PUB.psp: *
- 12: /cgn2_6/ptodata/2/pubpaa/us10_PUBCOMB.psp: *
- 13: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB.psp: *
- 14: /cgn2_6/ptodata/2/pubpaa/us60_PUBCOMB.psp: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	406.5	18.2	135	10	US-09-788-074-1	Sequence 1, Appl
2	350.5	15.7	135	10	US-09-788-074-3	Sequence 3, Appl
3	189.5	8.5	132	10	US-09-501-436A-11	Sequence 11, Appl
4	174.5	7.8	132	10	US-09-505-235-1	Sequence 1, Appl

ALIGNMENTS

```

RESULT 1
US-09-788-074-1
; Sequence 1, Application US/09788074
; Patent No. US2001004110A1
; GENERAL INFORMATION:
; APPLICANT: Hotamisligil, Gokhan S. MAIL
; TITLE OF INVENTION: INHIBITION OF MALL
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-074-1

```

Alignment Scores:	
Pred. No.:	5, 43e-36
Score:	406.50
Length:	135
Percent Similarity:	45.02%
Matches:	93
Best Local Similarity:	44.08%
Conservative:	2
Query Match:	18.16%
Mismatches:	6
Indels:	110
DB:	10
Gaps:	1

Sequence 2, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 15, Appl
Sequence 38, Appl
Sequence 428, Appl
Sequence 496, Appl
Sequence 14, Appl
Sequence 48, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 49, Appl
Sequence 8, Appl
Sequence 91, Appl
Sequence 98, Appl
Sequence 2, Appl
Sequence 177946, Appl
Sequence 74, Appl
Sequence 5, Appl
Sequence 1072, Appl
Sequence 2, Appl
Sequence 85, Appl
Sequence 1393, Appl
Sequence 92, Appl
Sequence 94, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 9, Appl
Sequence 806, Appl
Sequence 2, Appl
Sequence 434, Appl
Sequence 17, Appl
Sequence 96, Appl

US-09-788-074-2 (1-1279) x US-09-788-074-1 (1-135)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACACTGTATCATACG 190
 Db 27 GlyValGlyLeuAlaLeuArgLysMetAlaLaMetAlaLysProAspCysIleIlethr 46
 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyAsnAsnIleThrValLysThrGluSerThrValLysThrValPheSer 66
 QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGATGGCAGAAAACACTGAGGTACG 310
 Db 67 CysAsnLeuGlyLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
 QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTACAGATTAAATTGCATTAAACAT 370
 Db 85 ----- 85
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 85 ----- 85
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACATCTTATGAGTTCTAGATCGAAAA 490
 Db 85 ----- 85
 QY 491 GCACATAGTTGTATTCTGAACAAAATCAGTATGATGGGTGGAGTTCACAGAGGGAAGG 550
 Db 85 ----- 85
 QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTTCACTTTGAAGATGATGAAC 610
 Db 85 ----- 85
 QY 611 TAACACCTGTATTCTTTCAGACAGCTGTGCACCTTCCAAAGCGTGCCTCGTCACGCA 670
 Db 86 -----ValCysThrPheGlnAspGlyAlaLeuValGlnhi 97
 QY 671 CCAGCAATGGGCGGAGGAGGACGACGATACAGAAAACACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetIi 117
 QY 731 CGTGTGTGACATCAAGCACTGGCCACCATGC 761
 Db 117 eValGluCysValMetAsnAlaThrCys 127

RESULT 2

US-09-788-074-3
 ; Sequence 3, Application US/09788074
 ; Patent No. US20010044110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hotamisligil, Gokhan S.
 ; TITLE OF INVENTION: INHIBITION OF MAL1
 ; FILE REFERENCE: 21509-044
 ; CURRENT APPLICATION NUMBER: US/09/788,074
 ; CURRENT FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,106
 ; PRIOR FILING DATE: 2000-02-17
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-788-074-3

Alignment Scores:
 Pred. No.: 6.34e-30 Length: 135
 Score: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-788-074-3 (1-135)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACACTGTATCATACG 190
 Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIlethr 46
 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
 QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGATGGCAGAAAACACTGAGGTACG 310
 Db 67 CysThrLeuGlyLysPheGluThrThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTACAGATTAAATTGCATTAAACAT 370
 Db 84 ----- 84
 QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 Db 84 ----- 84
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACATCTTATGAGTTCTAGATCGAAAA 490
 Db 84 ----- 84
 QY 491 GCACATAGTTGTATTCTGAACAAAATCAGTATGATGGGTGGAGTTCACAGAGGGAAGG 550
 Db 84 ----- 84
 QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCTGGGGTTCCTTTCACTTTGAAGATGATGAAC 610
 Db 84 ----- 84
 QY 611 TAACACCTGTATTCTTTCAGACAGCTGTGCACCTTCCAAAGCGTGCCTCGTCACGCA 670
 Db 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnhi 97
 QY 671 CCAGCAATGGGCGGAGGAGGACGACGATACAGAAAACACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGTGACATCAAGCACTGGCCACCATGC 761
 Db 117 iValGluCysValMetAsnValThrCys 127

RESULT 3

US-09-901-436A-11
 ; Sequence 11, Application US/09901436A
 ; Patent No. US20020098515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NI et al.
 ; TITLE OF INVENTION: Cytostatin I
 ; FILE REFERENCE: PFI75D4
 ; CURRENT APPLICATION NUMBER: US/09/901,436A
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 09/361,737
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: 09/023,073
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 08/470,298
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: 08/409,731
 ; PRIOR FILING DATE: 1995-03-24
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: human
 US-09-901-436A-11

Alignment Scores:

Pred. No.: 1.74e-12 Length: 132
 Score: 189.50 Matches: 53
 Percent Similarity: 34.33% Conservative: 16
 Best Local Similarity: 26.37% Mismatches: 22
 Query Match: 8.46% Indels: 110
 DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-901-436A-11 (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
 DB 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer 44
 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCCAGAGACACAGTGAAGACGACTGTGTCTCT 250
 DB 45 LysLysGlyAspIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64
 QY 251 TCTAACCTGGGAGAGAAAGTTTCATCAAAACCCAGAGACACAGTGGCAGAAAACCTGAGTCAGC 310
 DB 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSer-- 83
 QY 311 TACAACATACCTGTGAAGCCAGACAAAGCTTCTAGATTACAGATTAAATTGCATTAAACAAT 370
 DB 83 ----- 83
 QY 371 GTCCTGCTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 DB 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 DB 83 ----- 83
 QY 491 GCACATAGTTGTTGATGTGAACAAATCAGTATGATGGGTGCGAGTTCAGAGAGGAAAGG 550
 DB 83 ----- 83
 QY 551 CGAAGACTGTTGAGTGGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 DB 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACAGCGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
 DB 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95
 QY 671 CCAGCAATGGGACGGAGGAGCAGCAGTAAACAAGAACTGAAGGATGGGAAGATGAT 730
 DB 95 GlnArgTrpaspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
 QY 731 C 731
 DB 115 I 115

RESULT 4

US-09-905-235-1
 ; Sequence 1, Application US/09905235
 ; Patent No. US20020035064A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 ; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND COMBI
 ; FILE REFERENCE: LA24a
 ; CURRENT APPLICATION NUMBER: US/09/905.235
 ; CURRENT FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-905-235-1

Alignment Scores:

Pred. No.: 1.74e-12 Length: 132
 Score: 189.50 Matches: 53
 Percent Similarity: 34.33% Conservative: 16
 Best Local Similarity: 26.37% Mismatches: 22
 Query Match: 8.46% Indels: 110
 DB: 10 Gaps: 1

Pred. No.: 7.36e-11 Length: 132

Score: 174.50 Matches: 50
 Percent Similarity: 32.67% Conservative: 16
 Best Local Similarity: 24.75% Mismatches: 26
 Query Match: 7.79% Indels: 110
 DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-905-235-1 (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTCAG 190
 DB 25 GlyValGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer 44
 QY 191 TGTGATGGCAACAACATCACGGTCAAAACCCAGAGACACAGTGAAGACGACTGTGTCTCT 250
 DB 45 ValAsnGlyAspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer 64
 QY 251 TCTAACCTGGGAGAGAAAGTTTCATCAAAACCCAGAGACACAGTGGCAGAAAACCTGAGTCAGC 310
 DB 65 PheIleLeuGlyGlnGluPheAspGluValThrAlaAspAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCCAGACAAAGCTTCTAGATTACAGATTAAATTGCATTAAACAAT 370
 DB 83 ----- 83
 QY 371 GTCCTGCTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
 DB 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
 DB 83 ----- 83
 QY 491 GCACATAGTTGTTGATGTGAACAAATCAGTATGATGGGTGCGAGTTCAGAGAGGAAAGG 550
 DB 83 ----- 83
 QY 551 CGAAGACTGTTGAGTGGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 DB 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACAGCGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
 DB 84 -----ThrIleThrLeuAspGlyValLeuValHisVa 95
 QY 671 CCAGCAATGGGACGGAGGAGCAGCAGTAAACAAGAACTGAAGGATGGGAAGATGAT 730
 DB 95 GlnArgTrpaspGlyLysSerThrThrIleLysArgLysArgGluAspAspLysLeuVa 115
 QY 731 C 734
 DB 115 I 116

RESULT 5

US-09-986-240-2
 ; Sequence 2, Application US/09986240
 ; Patent No. US20020119496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weigelt, Johan
 ; APPLICANT: Wikström, Mats
 ; TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
 ; FILE REFERENCE: METHOD
 ; CURRENT APPLICATION NUMBER: US/09/986,240
 ; CURRENT FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: 60/243,626
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: SE 0003811-7
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 132

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-240-2

Alignment Scores:
Pred. No.: 1.56e-10 Length: 132
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-986-240-2 (1-132)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGCAGCTGTATCATTCAG 190
Db 24 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 43
QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 44 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelysAsnThrGlulileSer 63
QY 251 TGTAACTGGGAGAGAAAGTTTATGAACACGACGCTGATGGCAGAAAACACTGAGGTTCAGC 310
Db 64 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 82
QY 311 TACAACATACCTGTGAAGCGCACAGAAGCTTCTAGATTACAGATTAAATTGCATTAAACAT 370
Db 82 ----- 82
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 82 ----- 82
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 82 ----- 82
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 82 ----- 82
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 82 ----- 82
QY 611 TAACATACCTGTATTTTCCAGACGGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
Db 83 ----- 83
QY 671 CCAGCAATGGGAGCGGAGGAGGACGACGATAACAGAAAACCTGAAGGATGGAAGATGAT 730
Db 94 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeu11 114
QY 731 CGTGGTGAACATCAAGACACTGGCACCATGC 761
Db 114 eLeuThrLeuThrHisGlyThrAlaValCys 124

RESULT 6

US-09-901-436A-10
; Sequence 10, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PFI75D4
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298

; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-10

Alignment Scores:

Pred. No.: 1.56e-10 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-901-436A-10 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGCAGCTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 44
QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelysAsnThrGlulileSer 64
QY 251 TGTAACTGGGAGAGAAAGTTTATGAACACGACGCTGATGGCAGAAAACACTGAGGTTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACCTGTGAAGCGCACAGAAGCTTCTAGATTACAGATTAAATTGCATTAAACAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACATACCTGTATTTTCCAGACGGTCTGCACCTTCCAGACGGTGCCTGGTCCAGCA 670
Db 84 ----- 84
QY 671 CCAGCAATGGGAGCGGAGGAGGACGACGATAACAGAAAACCTGAAGGATGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeu11 115
QY 731 CGTGGTGAACATCAAGACACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 7

US-10-153-740-13
; Sequence 13, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.

;; DILLON, PATRICK
;; TITLE OF INVENTION: CYTOSTATIN III
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;; STREET: 9410 KEY WEST AVENUE
;; CITY: ROCKVILLE
;; STATE: MD
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/153,740
;; FILING DATE: 24-May-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/734,036
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 09/307,817
;; FILING DATE: <Unknown>
;; * ATTORNEY/AGENT INFORMATION:
;; NAME: BROOKES, ANDERS A.
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PF222
;; TELECOMMUNICATION INFORMATION:
;; * TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 133 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; * MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-153-740-13

Alignment Scores:
Pred. No.: 1,56e-10 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-13 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCAGCTGTATCATTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIlelleGlu 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCCGAGACACAGTCAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAAGAAAACACTGAGGTTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTTCACAGATTAAATTCGATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490

Db 83 ----- 83
QY 491 GCACATAGTTGATTGTTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGCTGGGGTTCCTTCACTTTGGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCCTGTATTTTTCGACAGCGTCTGCACCTTCCAAGACGGTCCCTGTGTCAGCA 670
Db 84 -----IleValThrLeuAspGlyGlyLysLeuValHisLe 95
QY 671 CCAGCAATGGGACGGGAAGAGAGACGACGATACAAAGAAAACACTCAAGGATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuI 115
QY 731 CGTGGTGAGCATCAAGACACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
RESULT 8
US-09-901-436A-7
; Sequence 7, Application US/09901436A
; Patent No. US20020098515A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Cytostatin I
; FILE REFERENCE: PF17504
; CURRENT APPLICATION NUMBER: US/09/901,436A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/361,737
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/023,073
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/470,298
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/409,731
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO: 7
; LENGTH: 133
; TYPE: PRT
; ORGANISM: human
US-09-901-436A-7
Alignment Scores:
Pred. No.: 1.15e-09 Length: 133
Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 10 Gaps: 1
US-09-788-074-2 (1-1279) x US-09-901-436A-7 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCAGCTGTATCATTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIlelleGlu 44
QY 191 TGTGATGGCAACAACATCATCGGTCAAAACCCGAGACACAGTCAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACGACAGCTGTATGGCAAGAAAACACTGAGGTTCAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTCTGAAGCCACAGAAGCTTCTAGATTTCACAGATTAAATTCGATTAACAAT 370
Db 83 ----- 83

```
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAGAACTACTTTATGGAGTTGATGATA 430
Db 83 -----
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 -----
QY 491 GCACATAGTTGTATTCTGAACAAATCAGTATGATGGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 -----
QY 551 CGAAGACTTGTGGAGTGTGGTCTCTGGGGTTCCTTACATTGGAAGATGATGAAC 610
Db 83 -----
QY 611 TAACCTACCTGTATTTTCCAGACGGTCTGCACCTTCCAGACGGTCCCTGGTCCAGCA 670
Db 84 -----
QY 671 CCAGCAATGGAGGAGGAGGAGCAGCAGTAAACAAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnLysTrpAsnGlyGlnGluThrLeuThrArgGluLeuValAspGlyLysLeu 115
QY 731 CGTG 734
Db 115 eLeu 116

RESULT 9
US-10-153-740-11
; Sequence 11, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-153-740-11

Alignment Scores:
Pred. No.: 1.15e-09 Length: 133
Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-11 (1-133)
QY 131 GGAGTAGGACTGGCTTTAGGAAGATGGCTGCATGGCCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrLeuLeuGlu 44
QY 191 TGTGATGGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluLeuAsn 64
QY 251 TGTAACTGGGAGAGAAGTTTGATGAACAGCAGCTGATGGCAGAAAAAAGTGAAGTCAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTCTGAAGCGAGAGAACCTTCTAGATTACAGATTAAATTGCATTACAAT 370
Db 83 -----
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 -----
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACATCTTATGAGTTCTAGATCGAAAA 490
Db 83 -----
QY 491 GCACATAGTTGTATTGTGNACAAATCAGTATCATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 -----
QY 551 CGAAGACTTGTGGAGTGTGGTCTCTGGGGTTCCTTACATTGGAAGATGATGAAC 610
Db 83 -----
QY 611 TAACCTACCTGTATTTTTCAGACGGTCTGCACCTTCCAGACGGTCCCTGGTCCAGCA 670
Db 84 -----
QY 671 CCAGCAATGGGAGGAGGAGGAGCAGCAGTAAACAAAGAACTGAAGGATGGGAAGATGAT 730
Db 95 lGlnLysTrpAsnGlyGlnGluThrLeuThrArgGluLeuValAspGlyLysLeu 115
QY 731 CGTG 734
Db 115 eLeu 116

RESULT 10
US-10-153-740-12
; Sequence 12, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
```


CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,740
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/734,036
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/307,817
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-740-12

Alignment Scores:
Pred. No.: 4e-09 Length: 133
Score: 158.50 Matches: 45
Percent Similarity: 31.28% Conservative: 21
Best Local Similarity: 21.33% Mismatches: 35
Query Match: 7.08% Indels: 110
DB: 12 Gaps: 1

US-09-788-074-2 (1-1279) x US-10-153-740-12 (1-133)

```
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGCAGACTGAAGACGACTGTGTCTCT 250
Db 45 ValAsnGlyAspThrValIleIleLysThrGlnSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTTCAGATTAAATTGCAATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGTGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 83 ----- 83
```

```
QY 551 CGAAGACTTGTGGAGTGGTGTGGGTCCCTGGGGGTTCTTCCTTCTTGGAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTATTTTGCAGACAGCGTGTGCACCTTCCAAAGACGGTGCCCTGCTCCAGCA 670
Db 84 -----IleValThrLeuAspGlyGlyLysLeuValHisVa 95
QY 671 CCAGCAATGGGACGGGAAGAGAGACGACGATACAAAGAACTGAAGAGTGGGAGATGAT 730
Db 95 lGlnLysTrpAsnGlyGlnGluThrSerLeuValArgGluMetValAspGlyLysLeuIl 115
QY 731 CGTGGTGCAGCATCAAAACGACTGCCACCATCC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
RESULT 11
US-09-971-187-2
; Sequence 2, Application US/09971187
; Patent No. US20020031804A1
; GENERAL INFORMATION:
; APPLICANT: Jian Ni et al.
; TITLE OF INVENTION: Cytostatin II
; FILE REFERENCE: PF221D1
; CURRENT APPLICATION NUMBER: US/09/971,187
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/043,646
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/US95/12540
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: human
US-09-971-187-2
Alignment Scores:
Pred. No.: 2.29e-08 Length: 132
Score: 151.50 Matches: 48
Percent Similarity: 32.51% Conservative: 18
Best Local Similarity: 23.65% Mismatches: 25
Query Match: 6.77% Indels: 112
DB: 10 Gaps: 4
US-09-788-074-2 (1-1279) x US-09-971-187-2 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrValIleIleSer 44
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGAGCAGACTGAAGACGACTGTGTCTCT 250
Db 45 GlnGluGlyAspLysValIleIleArgThrLeuSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 65 PheGlnLeuGlyGluGluPheAspGluThrThrAlaAspArg----- 79
QY 311 TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTTCAGATTAAATTGCAATTAACAAT 370
Db 80 -----AsnCys----- 81
QY 371 GTCTGTACTTACTGCCAAGGGTGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 81 ----- 81
QY 431 AATTAGTAAAGTCCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAAA 490
Db 82 -----Lys 82
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
```

Db 83 Ser-ValValSerLeu----- 87
QY 551 CGAAGACTTGTGGAGTGTGGTCTGGGGTTCCTTCACCTTTTGAAGATGATGAAC 610
Db 87 ----- 87
QY 611 TAACTACCTGTATTTTTCAGAGCGGTCTGCACCTTCCAAAGCGGT---GCCCTGGTCCA 667
Db 88 -----AspGlyAspLysLeuValHi 94
QY 668 GCACCAGCAATGGACGGGGAAGAGACGACGATACACAGAACTGAAGATCGGAAGAT 727
Db 94 sileGlnLysTrpAspGlyLysGluThrAsnPheValArgGluLeuLysAspGlyLysMe 114
QY 728 GATCGTG 734
Db 114 tValMet 116
RESULT 12
US-10-153-740-15
; Sequence 15, Application US/10153740
; Patent No. US20020147149A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; YU, GUO-LIANG
; GENTZ, REINER L.
; DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,740
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,036
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,817
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-153-740-15
Alignment Scores:
Pred. No.: 4 01e-07 Length: 131
Score: 140.00 Matches: 48
Percent Similarity: 32.02% Conservative: 17
Best Local Similarity: 23.65% Mismatches: 25

Query Match: 6.25% Indels: 113
DB: 12 Gaps: 5
US-09-788-074-2 (1-1279) x US-10-153-740-15 (1-131)
QY 131 GGAGTAGGACTGCTCTTTAGGAAGATGGCTGCATATGCCAAGCCAGACTGTATCATTCAG 190
Db 25 GlyValGlyPheAlaThrArgGlnValGlyAsnValThrLysProThrValIleIleSer 44
QY 191 TGTGATGGCAACAACATCACGGTCAAACCCGAGAGACAGTGAAGACGACTGTGTTCTCT 250
Db 45 GlnGluGlyAspLysValIleArgThrLeuSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAAAACCTGAGTCA 310
Db 65 PheGlnLeuGlyGlu---PheAspGluThrThrAlaAspAspArg----- 78
QY 311 TACAACATACTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAATTCATTAACAAT 370
Db 79 -----AsnCys----- 80
QY 371 GTCGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 80 ----- 80
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTTATGAGTTCTAGATCGAAAA 490
Db 81 -----Lys 81
QY 491 GCACATAGTTGTATTGTGAACAAATACGATATGATGGGTGGAGTTCAGAGAGGAAAG 550
Db 82 Ser-ValValSerLeu----- 86
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTCGGGTCTTCCTTCACCTTTTGAAGATGATGAAC 610
Db 86 ----- 86
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGT---GCCCTGGTCCA 667
Db 87 -----AspGlyAspLysLeuValHi 93
QY 668 GCACCAGCAATGGACGGGGAAGAGACGACGATACACAGAACTGAAGATCGGAAGAT 727
Db 93 sileGlnLysTrpAspGlyLysGluThrAsnPheValArgGluLeuLysAspGlyLysMe 113
QY 728 GATCGTG 734
Db 113 tValMet 115
RESULT 13
US-09-925-301-848
; Sequence 848, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 848
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-925-301-848

Alignment Scores:

Pred. No.: 6,39e-05 Length: 160
Score: 120.00 Matches: 30
Percent Similarity: 60.61% Conservative: 10
Best Local Similarity: 45.45% Mismatches: 23
Query Match: 5.36% Indels: 3
DB: 10 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-925-301-848 (1-160)

QY 131 GGAGTAGGACTGGCTCTTAGGAAG-----ATGGTGCCATGGCCAAAGCCAGACTGTATC 184
Db 47 GlyValAsnAlaMetLeuArgLysValAlaValAlaAlaSerLysProHisValGlu 66
QY 185 ATTACGTGTGGGCAACAACATCAGCGTCAAAACCGAGAGCAGACTGAAGAGCACTGTG 244
Db 67 IleArgGlnAspGlyAspGlnPheThrValArgThrThrValArgThrThrGlu 86
QY 245 TTCTCTTTAACTGGGAGAGAGTTTGTATGAACAGCAGCTGATGGCAGAAAAAAGTGA 304
Db 87 IleAsnPheLysValGlyGluGluPheGluGluThrValAspGlyArg-LysCysar 106
QY 305 GTCAGCTACACATAC 320
Db 106 gSerLeuAlaThrTrp 111

RESULT 14

US-09-736-457-328

; Sequence 328, Application US/09736457

; Patent No. US20020168637A1

; GENERAL INFORMATION:

; APPLICANT: Wang, TongLong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Lijun

; APPLICANT: Wang, Aljun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736,457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 328

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-736-457-328

Alignment Scores:

Pred. No.: 9,92e-05 Length: 138
Score: 118.00 Matches: 28
Percent Similarity: 61.04% Conservative: 19
Best Local Similarity: 36.36% Mismatches: 22
Query Match: 5.27% Indels: 8
DB: 9 Gaps: 2

US-09-788-074-2 (1-1279) x US-09-736-457-328 (1-138)

QY 71 ATGATAAGGAATGAATCCTTGTATCATTTGACAAATTCAGTCTTTTCCATACCCACA 130
Db 10 IleIleArgSerGluAsnPheGluGluLeuLeuLysVal-----Leu 23
QY 131 GGAGTAGGACTGGCTCTTAGGAAG-----ATGGTGCCATGGCCAAAGCCAGACTGTATC 184
Db 24 GlyValAsnValMetLeuArgLysIleAlaValAlaAlaSerLysProAlaValGlu 43

QY 185 ATTACGTGTGTGGCAACAACATCAGCGTCAAAACCGAGAGCAGACTGAAGAGCACTGTG 244
Db 44 IleLysGlnGluGlyAspThrPheThrIleLysThrSerThrValArgThrThrGlu 63
QY 245 TTCTCTTTAACTGGGAGAGAGTTTGTATGAACAGCAGACTGTATGGGCAGA 295
Db 64 IleAsnPheLysValGlyGluGluPheGluGluGlnThrValAspGlyArg 80
RESULT 15
US-09-925-302-496
; Sequence 496, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 496
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-496

Alignment Scores:

Pred. No.: 0.000102 Length: 149
Score: 118.00 Matches: 28
Percent Similarity: 61.04% Conservative: 19
Best Local Similarity: 36.36% Mismatches: 22
Query Match: 5.27% Indels: 8
DB: 10 Gaps: 2

US-09-788-074-2 (1-1279) x US-09-925-302-496 (1-149)

QY 71 ATGATAAGGAATGAATCCTTGTATCATTTGACAAATTCAGTCTTTTCCATACCCACA 130
Db 21 IleIleArgSerGluAsnPheGluGluLeuLeuLysVal-----Leu 34
QY 131 GGAGTAGGACTGGCTCTTAGGAAG-----ATGGTGCCATGGCCAAAGCCAGACTGTATC 184
Db 35 GlyValAsnValMetLeuArgLysIleAlaValAlaAlaSerLysProAlaValGlu 54
QY 185 ATTACGTGTGTGGCAACAACATCAGCGTCAAAACCGAGAGCAGACTGAAGAGCACTGTG 244
Db 55 IleLysGlnGluGlyAspThrPheThrIleLysThrSerThrValArgThrThrGlu 74
QY 245 TTCTCTTTAACTGGGAGAGAGTTTGTATGAACAGCAGACTGTATGGGCAGA 295
Db 75 IleAsnPheLysValGlyGluGluPheGluGluGlnThrValAspGlyArg 91

Search completed: November 25, 2002, 10:34:31

Job time : 15.5 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 25, 2002, 10:25:53 ; Search time 17.5 Seconds
(without alignments)
4300.791 Million cell updates/sec

Title: US-09-788-074-2

Perfect score: 2239

Sequence: 1 aatgggagcaatgctagc.....tctatgagaagtcaatga 1279

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0		0.5	
Fgapop 6.0			7.0
Delop 6.0			

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_pool/US09788074/runat_25112002_093515_15707/app_query.fasta_1.1415
-DB=Issued Patents_AA -QMT=fastan -SUPFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09788074 -ECGN_1_17 @runat_25112002_093515_15707 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Issued Patents_AA:*

```
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	350.5	15.7	135	1	US-08-446-600A-4
2	189.5	8.5	132	1	US-08-409-731A-11
3	189.5	8.5	132	2	US-08-470-298B-11
4	189.5	8.5	132	2	US-09-023-073A-11
5	189.5	8.5	132	4	US-09-361-737-11
6	171.5	7.7	133	1	US-08-409-731A-10
7	171.5	7.7	133	2	US-08-470-298B-10
8	171.5	7.7	133	2	US-08-820-825-13
9	171.5	7.7	133	2	US-09-023-073A-10
10	171.5	7.7	133	4	US-09-307-817-13
11	171.5	7.7	133	4	US-09-361-737-10
12	171.5	7.7	133	4	US-09-734-036-13

```
13 163.5 7.3 131 1 US-08-409-731A-7
14 163.5 7.3 131 2 US-08-470-298B-7
15 163.5 7.3 133 2 US-08-820-825-11
16 163.5 7.3 133 2 US-09-023-073A-7
17 163.5 7.3 133 4 US-09-307-817-11
18 163.5 7.3 133 4 US-09-361-737-7
19 163.5 7.3 133 4 US-09-734-036-11
20 158.5 7.1 133 2 US-08-820-825-12
21 158.5 7.1 133 4 US-09-307-817-12
22 158.5 7.1 133 4 US-09-734-036-12
23 151.5 6.8 132 4 US-09-043-646-2
24 140 6.3 131 2 US-08-820-825-15
25 140 6.3 131 4 US-09-307-817-15
26 140 6.3 131 4 US-09-734-036-15
27 139.5 6.2 132 2 US-08-470-298B-12
28 120 5.4 137 1 US-08-468-709B-4
29 120 5.4 137 2 US-08-241-664B-4
30 120 5.4 137 5 PCT-US93-03936-4
31 119 5.3 137 1 US-08-468-709B-11
32 119 5.3 137 2 US-08-241-664B-11
33 118 5.3 138 1 US-08-468-709B-2
34 118 5.3 138 2 US-08-241-664B-2
35 118 5.3 138 5 PCT-US93-03936-2
36 109 4.9 133 1 US-08-554-463-1
37 108 4.8 138 1 US-08-468-709B-12
38 108 4.8 138 2 US-08-241-664B-12
39 104 4.6 135 2 US-08-820-825-2
40 104 4.6 135 4 US-09-307-817-2
41 104 4.6 135 4 US-09-734-036-2
42 102 4.6 135 1 US-08-409-731A-8
43 102 4.6 135 2 US-08-470-298B-8
44 102 4.6 135 2 US-08-847-724-4
45 102 4.6 135 2 US-08-847-724-6
```

ALIGNMENTS

RESULT 1

US-08-446-600A-4
; Sequence 4, Application US/08446600A
; Patent No. 5719126

; GENERAL INFORMATION:

; APPLICANT: No. 5719126dlund, James J. and Farooqui, Jamal Z.

; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Frost & Jacobs

; STREET: 2500 PNC Center, 201 East Fifth St.

; CITY: Cincinnati

; STATE: OH

; COUNTRY: USA

; ZIP: 45202-4182

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,600A

; FILING DATE: 24 May 1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/980,513

; FILING DATE: 24 No. 5719126member 1992

; APPLICATION NUMBER: PCT/US93/11139

; FILING DATE: 16 No. 5719126member 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Ann G. Robinson

; REGISTRATION NUMBER: 39,820

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 651-6128

; TELEFAX: (513) 651-6981

TELEX: 21-4396 F&J Cin
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
US-08-446-600A-4

Alignment Scores:
Pred. No.: 1,14e-32 Length: 135
Score: 350.50 Matches: 78
Percent Similarity: 41.71% Conservative: 10
Best Local Similarity: 36.97% Mismatches: 13
Query Match: 15.65% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-446-600A-4 (1-135)

QY 131 GGAGTAGGACTGCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTACG 190
Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACATACAGCTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAAACACTGAGTCAAGC 310
Db 67 CysThrLeuGlyGlyLysPheGluThrThrAlaAspGlyArgLysThr-Gln----- 84
QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCGATTAAACAAT 370
Db 84 ----- 84
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGTAAGAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 84 ----- 84
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 84 ----- 84
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 84 ----- 84
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTGGTCTGGGGTCTTCTACTTTGGAAGATGATGAAC 610
Db 84 ----- 84
QY 611 TAACTACCTGTATTTTTCACAGCGTCTGCACCTTCCAAGACGFTGCCCTGGTCCAGCA 670
Db 85 -----ThralcysasnPheThrAspGlyAlaLeuValGlnH1 97
QY 671 CCAGCAATGGGAGGAGGAGCAGCAGTAAACAGAAACTGAAGGATGGGAAGATGAT 730
Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
QY 731 CGTGTGACATCAAGACTGGCACCATGC 761
Db 117 lValGluCysValMetAsnAsnValThrCys 127

RESULT 2
US-08-409-731A-11
; Sequence 11, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PE175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-409-731A-11

Alignment Scores:
Pred. No.: 1.02e-13 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-409-731A-11 (1-132)

QY 131 GGAGTAGGACTGCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTACG 190
Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer 44
QY 191 TGTGATGGCAACATACAGCTCAAAACCGAGACACAGTGAAGACGACTGTGTCTCT 250
Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAAACACTGAGTCAAGC 310
Db 65 PheLysLeuGlyGlnGluPheGluGluThrThrAlaAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCGATTAAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGTAAGAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTGGGGTCTTCTACTTTGGAAGATGATGAAC 610

```
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTGCAGACGGTCTGCACCTTCCAAAGACGGTGCCTGTGTCACGCA 670
Db 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95
QY 671 CCAGCAATGGGACGGAGGAGGACGATACACAGAACTGAAGATGGGAAGATGAT 730
Db 95 lGlnArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 C 731
Db 115 I 115

RESULT 3
US-08-470-298B-11
; Sequence 11, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MYELIN P2 (FIGURE 2)
US-08-470-298B-11

Alignment Scores:
Pred. No.: 1.02e-13 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-470-298B-11 (1-132)
QY 131 GCAGTAGGACTGCCTCTTAGGAGATGGCTGCCATGCCCAAGCCAGACGTATCATTCAG 190
Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleIleSer 44
```

```
QY 191 TCTGATGGCAACAACATCATCGGTCAAAACCCGAGACGACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysLysGlyAspIlelleThrIleArgThrGluSerThrPhelYasnThrGluIleSer 64
QY 251 TCTAACTCTGGGAGAGAAAGTTTGTATGAACGACAGCTGTGGCAGAAAACACTGAGGTCAAC 310
Db 65 PheLysLeuGlyGlnGluPheGluGluThrIleAlaAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACACTACTGTGAAGCGACGACGAAGCTTCTAGATTTCACAGATTAAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGCTCCCGAGCACTAAGAAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTATTGTGAACAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGCTGTGTGGTCTCTGGGGTTCCTTCACTTTTGGAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTGCCTGTGTCACGCA 670
Db 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95
QY 671 CCAGCAATGGGACGGAGGACGACGATACACAGAAAACACTGAAGATGGGAAGATGAT 730
Db 95 lGlnArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 C 731
Db 115 I 115

RESULT 4
US-09-023-073A-11
; Sequence 11, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,073A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43, 975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
```

```
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-023-073A-11

Alignment Scores:
Pred. No.: 1 02e-13 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservatives: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-023-073A-11 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGCCAAGCCAGACTGTATCATTCACG 190
Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleSer 44
QY 191 TGTGATGGCAACAATCATCGGTCAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAACTGAGGTCAGC 310
Db 65 PheLysLeuGlyGlnGluPheGluGluThrAlaAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACATACCTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAATAATGCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGATTGTGTAACAAATACATATGATGGGCTGGAGTTCACAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGGTGGGCTGCTGCACCTTCCAAAGAGGTCCTGTCACATTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTGCAGACGGTCTGCACCTTCCAAAGAGGTCCTGTCACGACGA 670
Db 84 -----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95
QY 671 CCAGCAATGGGACGGAGGAGGACGATAAACAAGAAACTGAAGGATGGGAAGATGAT 730
Db 95 IGLNArgTrpaspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 C 731
Db 115 1 115

RESULT 5
US-09-361-737-11
; Sequence 11, Application US/09361737
; Patent No. 6287812
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
```

```
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,737
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,073
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: P-43,975
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-361-737-11

Alignment Scores:
Pred. No.: 1 02e-13 Length: 132
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservatives: 16
Best Local Similarity: 26.37% Mismatches: 22
Query Match: 8.46% Indels: 110
DB: 4 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-361-737-11 (1-132)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTCACG 190
Db 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleSer 44
QY 191 TGTGATGGCAACAATCATCGGTCAAACCGAGAGCACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysLysGlyAspIleIleThrIleArgThrGluSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAAGAACTGAGGTCAGC 310
Db 65 PheLysLeuGlyGlnGluPheGluGluThrAlaAspAsnArgLysThr-LysSer-- 83
QY 311 TACAACATACCTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAATAATGCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGATTGTGTAACAAATACATATGATGGGCTGGAGTTCACAGAGGGAAGG 550
```


TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: FABP (FIGURE 2)
ORGANISM: FABP (FIGURE 2)
US-08-470-298B-10

Alignment Scores:
Pred. No.: 1,35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-470-298B-10 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTCACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACAGCAGTGAAGCAGCTGTGTTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTGGCAGAAAACTGAGGTGACG 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysvalLysSer-- 83
QY 311 TACAACATAGTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAATAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGGTCCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACACTCCCTGTATTTTGCACAGCGTCTGCACCTTCCAAAGAGCGTCCCTGTCAGCA 670
Db 84 ----- 83
QY 671 CCAGCAATGGGCGGAGAGACAGATACAGAAAACTGAAGGATGGGAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuIle 115
QY 731 CGTGGTGAGCATCAAGAGCTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 8
US-08-820-13
Sequence 13, Application US/08820825
Patent No. 5945309
GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-820-825-13

Alignment Scores:
Pred. No.: 1,35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-820-825-13 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTCACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACAGCAGTGAAGCAGCTGTGTTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTGGCAGAAAACTGAGGTGACG 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysvalLysSer-- 83
QY 311 TACAACATAGTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAATAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTGTATTGTGTGAACAAAAATCAGATATGATGGGTGGAGTTTCAGAGAGGAAAGG 550

Db	83	-----83	
Qy	551	CGAAGACTTGTTGGACTGGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC	610
Db	83	-----83	
Qy	611	TAACTACCTGTATTTTTCGAGACGGCTCTGCACCTTCCAAGACGGTGCCTCGTCCAGCA	670
Db	84	-----TleValThrLeuAspGlyGlyLeuValHisLe	95
Qy	671	CCAGCAATGGGACGGGAAGGAGACGACGATAACACAAAACTGAAGCATGGGAAGATGAT	730
Db	95	uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuIle	115
Qy	731	CGTGGTGAGCATCAAAACGACTGGCACCATGC	761
Db	115	eLeuThrLeuThrHisGlyThrAlaValCys	125

```

RESULT 9
US-09-023-073A-10
; Sequence 10, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; *NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA

```

```

, ZIP: 20850
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/023,073A
, FILING DATE: 13-FEB-1998
, CLASSIFICATION: 424
, ATTORNEY/AGENT INFORMATION:
, NAME: Wales, Michele M.
, REGISTRATION NUMBER: P-43,975
, REFERENCE/DOCKET NUMBER: PF175D2
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 301-610-5772
, TELEFAX: 301-309-8439
, INFORMATION FOR SEQ ID NO: 10:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 133 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, US-09-023-073A-10

```

Alignment Scores:	
Pred. No.:	1,35e-11
Score:	171.50
Percent Similarity:	32.23%
Best Local Similarity:	23.70%
Query Match:	7.66%
DB:	2
Length:	133
Matches:	50
Conservative:	18
Mismatches:	33
Indels:	110
Gaps:	1

US-09-788-074-2 (1-1279) x US-09-023-073A-10 (1-133)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAGCCAGACTGTATCATACG 190

Db	25	GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrIleLeuGlu	44
Qy	191	TGTCATGGCAACATCATCGGTCAAAACCGAGACACAGTGAAGACGACTGTGTTCTCT	250
Db	45	LysAsnGlyAspIleLeuThrLeuThrHisSerThrPheLysAsnThrGluIleSer	64
Qy	251	TGTAACCTGGGACAGAGATTGATGAACACGACAGCTGATGGCAGAAAACTGAGGTCCAG	310
Db	65	PheLysLeuGValGluPheAspGluThrThrAlaAspArg-LysValLysSer	83
Qy	311	TACAACATACTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAAATTGCATTAAACAAT	370
Db	83	----	83
Qy	371	GTCTGTACTTACTGCCAAGGCTCACTGAAAAAACAATACTTTATGGAGTTGCATTTTGATA	430
Db	83	----	83
Qy	431	ANTTAGTAAAGTCCCAGGACTAAGAANTGAACACATCTTATCAGTTTCTAGATCGAAAA	490
Db	83	----	83
Qy	491	GCACATAGTTGATTGTGAACAAAATCAGTATCATGGGTGGAGTTTCAGAGAGGGAAGG	550
Db	83	----	83
Qy	551	CGAAGACTTGTGGAGTGGTGTGGGTCTGGGGTTCCTTCACTTTGGAAGATGATGAAC	610
Db	83	----	83
Qy	611	TAACACCTGTATTTTTTCAGACGGTCTGCACCTTCCAGACGGTCCCTGGTCCAGCA	670
Db	84	-----iLeValThrLeuAspGlyGlyLysLeuValHisLe	95
Qy	671	CCACATGGGACGGGAAGGAGACGACGATAAACAAGAAACTCAAGATGGGAAGATGAT	730
Db	95	uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuIle	115
Qy	731	CGTGGTGAGCATCAAGCACTGGCCACCATGC 761	
Db	115	eLeuThrLeuThrHisGlyThrAlaValCys 125	
RESULT 10			
US-09-307-817-13			
; Sequence 13, Application US/09307817			
; Patent No. 6232291			
; GENERAL INFORMATION:			
; APPLICANT: NI, JIAN			
; APPLICANT: YU, GUO-LIANG			
; APPLICANT: GENTZ, REINER L.			
; APPLICANT: DILLON, PATRICK			
; TITLE OF INVENTION: CYTOSTATIN III			
; NUMBER OF SEQUENCES: 15			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.			
; STREET: 9410 KEY WEST AVENUE			
; CITY: ROCKVILLE			
; STATE: MD			
; COUNTRY: USA			
; ZIP: 20850			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/307,817			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/820,825			
; FILING DATE:			

ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PE222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-307-817-13

Alignment Scores:
Pred. No.: 1,35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 4 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-307-817-13 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATCGCCAGCCAGACTGTATCATTCAG 190
DB 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGGCAACAACATCAGCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
DB 45 LysAsnGlyAspIleLeuThrLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACAGACAGCTGATGGCAAGAAACTGAGGTCAAC 310
DB 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCATTACAAT 370
DB 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
DB 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATCAGTTCTAGATCGAAA 490
DB 83 ----- 83
QY 491 GCACATAGTTGATTGTGAACAAAATCAGTATCATGGGTGGAGTTCAGAGAGGAAAGG 550
DB 83 ----- 83
QY 551 CGAAGACTGTGGAGTGTGTGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
DB 83 ----- 83
QY 611 TACTACCTGTATTTTGCAGACGGTCTGCACCTTCCAGACGGTGCCTGTCCAGCA 670
DB 84 -----TleValThrLeuAspGlyGlyLysLeuValHisLe 95
QY 671 CCAGCAATGGGAGGAGGACGACGATAAACAAGAAACTGAGGATGGGAAGATGAT 730
DB 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeu 115
QY 731 CGTGGTGAGCATCAAAAGCACTGGCACCATGC 761
DB 115 eLeuThrLeuThrHisGlyThrAlaValCys 125
RESULT 11
US-09-361-737-10
Sequence 10, Application US/09361737

Patent No. 6287812
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,073
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PE175D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-361-737-10

Alignment Scores:
Pred. No.: 1,35e-11 Length: 133
Score: 171.50 Matches: 50
Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 4 Gaps: 1

US-09-788-074-2 (1-1279) x US-09-361-737-10 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATCGCCAGCCAGACTGTATCATTCAG 190
DB 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
QY 191 TGTGATGGCAACAACATCAGCGTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
DB 45 LysAsnGlyAspIleLeuThrLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACAGACAGCTGATGGCAAGAAACTGAGGTCAAC 310
DB 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTCATTACAAT 370
DB 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
DB 83 ----- 83

QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCCGAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTTATCTGAACAAATACGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTTGGAGTGTGTGGTCCCTGGGGGTTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACAGCTGTCACCTTCCAGACGGTGCCTGGTCCAGCA 670
Db 84 -----11eValThrLeuAspGlyGlyLeuValHisLe 95
QY 671 CCAGCAATGGGAGGGAAGGAGCAGCATAACAAGAAACTGAAGCATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuII 115
QY 731 CGTGGTGAGCATCAAGCACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 12

US-09-734-036-13
; Sequence 13, Application US/09734036
; Patent No. 6413726
; GENERAL INFORMATION:
; *APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09734,036
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,817
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-734-036-13

Alignment Scores: 1.35e-11 Length: 133
Pred. No.: 171.50 Matches: 50
Score:

Percent Similarity: 32.23% Conservative: 18
Best Local Similarity: 23.70% Mismatches: 33
Query Match: 7.66% Indels: 110
DB: 4 Gaps: 1
US-09-788-074-2 (1-1279) x US-09-734-036-13 (1-133)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACTGTATCATTTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleLeuGlu 44
QY 191 TGTGATGGCAACACATCAGCGTCAAAACCGAGACACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysAsnGlyAspIleLeuThrLeuLysThrHisSerThrPhelLysAsnThrGluIleSer 64
QY 251 TGTAACTCTGGGAGAGAAGTTTGATGAACGACACAGCTGTAGTGGCAAAAACTGAGGTGAGC 310
Db 65 PheLysLeuGlyValGluPheAspGluThrThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCGACAGAGCTTCTTAGATTACAGATTAAATTCGATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATCAAGACATCTTATGAGTTTCTAGATCGAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGTTATTTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAG 550
Db 83 ----- 83
QY 551 CGAAGACTTTGGAGTGTGTGGTCCCTGGGGGTTCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACAGCTGTCACCTTCCAAGACGGTGCCTGGTCCAGCA 670
Db 84 -----11eValThrLeuAspGlyGlyLysLeuValHisLe 95
QY 671 CCAGCAATGGGAGGGAAGGAGCAGCAGCAGTAAACAAGAAACTGAAGCATGGGAAGATGAT 730
Db 95 uGlnLysTrpAspGlyGlnGluThrThrLeuValArgGluLeuIleAspGlyLysLeuII 115
QY 731 CGTGGTGAGCATCAAGCACTGGCACCATGC 761
Db 115 eLeuThrLeuThrHisGlyThrAlaValCys 125

RESULT 13

US-08-409-731A-7
; Sequence 7, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/409,731A
 FILING DATE: 24-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Robert H
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PF175
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8512
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-409-731A-7

Alignment Scores:
 Pred. No.: 1.17e-10 Length: 131
 Score: 163.50 Matches: 46
 Percent Similarity: 33.17% Conservative: 21
 Best Local Similarity: 22.77% Mismatches: 25
 Query Match: 7.30% Indels: 110
 DB: 1 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-409-731A-7 (1-131)

QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCAG 190
 Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
 QY 191 TGTGATGGCAACATACGCTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 45 LysAsnGlyAspThrIleThrLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
 QY 251 TGTAACTGGGAGAGAGTGTGATGAACCGACAGTGGCGAGAAACACTGAGTCAAC 310
 Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTGCATTACAAT 370
 Db 83 ----- 83
 QY 371 GTCTGTACTACTGCCAAGGGCTGACTGAAAAAATACTATTATGGAGTTGACTTTTGATA 430
 Db 83 ----- 83
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTTCTAGATCGAAA 490
 Db 83 ----- 83
 QY 491 GCACATAGTTGTATTGTGAACAAATACATGATGGGTGGAGTTTCAGAGAGGAAAGG 550
 Db 83 ----- 83
 QY 551 CGAAGACTTGTGGAGTGTGGTCCCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 83 ----- 83
 QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGTCCAGCA 670
 Db 84 -----LeuValThrLeuAspGlyGlyLysLeuIleHisVa 95
 QY 671 CCAGCAATGGGAGGAGGACGACGATACACAGAAACACTGAGGATGGGAAGATGAT 730
 Db 95 LGLysTrpAsnGlyGlnGluThrThrLeuThrArgGluLeuValAspGlyLysLeuI 115
 QY 731 CGTG 734
 |:::

Db 115 eLeu 116
 RESULT 14
 US-08-470-298B-7
 ; Sequence 7, Application US/08470298B
 ; Patent No. 5844081
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, REINER
 ; APPLICANT: YU, GUO-LIANG
 ; APPLICANT: ROSEN, CRAIG A.
 ; TITLE OF INVENTION: CYTOSTATIN I
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,298B
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ALLAN A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF175D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8512
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: MDGI (FIGURE 2)
 ; US-08-470-298B-7
 Alignment Scores:
 Pred. No.: 1.17e-10 Length: 131
 Score: 163.50 Matches: 46
 Percent Similarity: 33.17% Conservative: 21
 Best Local Similarity: 22.77% Mismatches: 25
 Query Match: 7.30% Indels: 110
 DB: 1 Gaps: 1
 US-09-788-074-2 (1-1279) x US-08-470-298B-7 (1-131)
 QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGCCCAAGCCAGACTGTATCATTCAG 190
 Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleGlu 44
 QY 191 TGTGATGGCAACATACGCTCAAAACCGAGACAGTGAAGACGACTGTGTCTCT 250
 Db 45 LysAsnGlyAspThrIleThrLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
 QY 251 TGTAACTGGGAGAGAGTGTGATGAACCGACAGTGGCGAGAAACACTGAGTCAAC 310
 Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
 QY 311 TACAACATACCTGTGAAGCGACAGAGCTTCTAGATTACAGATTAAATTGCATTACAAT 370
 Db 83 ----- 83

QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTTATGAGTTGACTTTTTCATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTGCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACAGCTCTGCACCTTCCAGACGGTCCCTGTGTCAGCA 670
Db 84 -----LeuValThrLeuAspGlyGlyLysLeuIleHisVa 95
QY 671 CGACCAATGGGACGGAAGAGAGACGATGATAACAAGAACTGAAGATGGGGAAGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrLeuThrArgGluLeuValAspGlyLysLeuIle 115
QY - 731 CGTG 734
Db 115 eLeu 116

RESULT 15

US-08-820-825-11
; Sequence 11, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/820,825

FILING DATE: 19-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF222

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-820-825-11

Alignment Scores:

Pred. No.: 1.18e-10 Length: 133

Score: 163.50 Matches: 46
Percent Similarity: 33.17% Conservative: 21
Best Local Similarity: 22.77% Mismatches: 25
Query Match: 7.30% Indels: 110
DB: 2 Gaps: 1

US-09-788-074-2 (1-1279) x US-08-820-825-11 (1-133)

QY 131 GGAGTAGGACTGCTCTTAGGAAGATGGCTGCCATGCCAAGCCAGACACTATCATTTACG 190
Db 25 GlyValGlyPheAlaThrArgGlnValAlaSerMetThrLysProThrThrIleIleGlu 44
QY 191 TGTGATGGCAACAACATCACGGTCAAAACGAGACAGACAGTGAAGACGACTGTGTTCTCT 250
Db 45 LysAsnGlyAspThrIleThrIleLysThrGlnSerThrPheLysAsnThrGluIleAsn 64
QY 251 TGTAACTGGGAGAGAAGTTTGTATGAACACGACAGCTGATGGCAGAAAACTAGAGTCAGC 310
Db 65 PheGlnLeuGlyIleGluPheAspGluValThrAlaAspArg-LysValLysSer-- 83
QY 311 TACAACATACTGTGAAGCCGACAGAGCTTCTAGATTTACAGATTAATTCATTAACAAT 370
Db 83 ----- 83
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTTATGAGTTGACTTTTTCATA 430
Db 83 ----- 83
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTTATGAGTTTCTAGATCGAAAA 490
Db 83 ----- 83
QY 491 GCACATAGTTGATTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGGAAGG 550
Db 83 ----- 83
QY 551 CGAAGACTTGTGGAGTGTGTGGTCTGCTGGGGTTCCTTCACTTTGGAAGATGATGAAC 610
Db 83 ----- 83
QY 611 TAACTACCTGTATTTTTCAGACAGGCTGCTGCACCTTCCAAAGACGGTCCCTGTGTCAGCA 670
Db 84 -----LeuValThrLeuAspGlyGlyLysLeuIleHisVa 95
QY 671 CCAGCAATGGGACGGAAGAGAGACGACGATACAAGAAACTGAAGATGGGGAAGATGAT 730
Db 95 LGlnLysTrpAsnGlyGlnGluThrLeuThrArgGluLeuValAspGlyLysLeuIle 115
QY 731 CGTG 734
Db 115 eLeu 116

Search completed: November 25, 2002, 10:34:01

Job time : 20.5 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: November 25, 2002, 10:24:12 ; Search time 61 Seconds
(without alignments)
5587.788 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 2239
Sequence: I aatgggagcaactctagc.....tctatgagaagtgcattga 1279

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p_model -DEV=xlp
-DB=/cgn2.1/USPTO_spool/US09788074/runat_25112002_093513_15657/app_query.fasta_1.1415
-LOOPEXT=0 -UNITS=dits -START=1 -END=1 -MATRIX=dlosum62 -TRANS=human40.cdi
-LIST=45 -LOCAL -OUTFMT=pto -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09788074.ecgn.1.1.43 @runat_25112002_093513_15657 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-FGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_101002:*
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	406.5	18.2	135	22	AAU08673
2	364.5	16.3	146	23	ABG60208
3	350.5	15.7	135	15	AAR55866
4	350.5	15.7	135	22	AAU08674
5	345.5	15.4	158	22	ABG27577
6	336.5	15.0	135	23	ABG61772
7	300.5	13.4	134	22	AAU08666
8	300.5	13.4	163	22	AAU08665
9	224	10.0	79	22	ABG13616
10	219	9.8	522	22	ABG13615
11	195	8.7	181	22	ABG13617
12	189.5	8.5	136	19	AAW40227
13	182	8.1	172	22	AAU10059
14	178	7.9	136	19	AAW40228
15	174.5	7.8	132	21	AAI90320
16	174.5	7.8	132	23	ABB08076
17	174	7.8	132	21	AAI90319
18	171.5	7.7	133	22	AAG66578
19	169.5	7.6	134	18	AAW31534
20	165.5	7.4	131	12	AAR13559
21	164.5	7.3	117	21	AAG03847
22	163.5	7.3	133	22	AAG66576
23	158.5	7.1	133	22	AAG66577
24	151.5	6.8	132	18	AAW22408
25	151.5	6.8	132	19	AAW80949
26	151.5	6.8	132	19	AAW81106
27	151.5	6.8	132	20	AAW82403
28	142.5	6.4	132	21	AAG03957
29	140	6.3	131	22	AAG66580
30	139.5	6.2	132	16	AAR75423
31	136	6.1	88	21	ABW58740
32	135	6.0	433	22	ABG27578
33	128	5.7	482	22	ABG18150
34	128	5.7	924	22	ABG13826
35	128	5.7	969	22	ABG24481
36	124	5.5	130	22	ABG62690
37	120	5.4	137	14	AAR42212
38	120	5.4	160	21	AAB43403
39	119	5.3	492	22	ABG28095
40	118	5.3	138	14	AAR42211
41	118	5.3	138	22	AAW76852
42	118	5.3	138	23	AAU85507
43	118	5.3	149	21	AAW58158
44	113	5.0	156	22	AAU02202
45	111.5	5.0	117	22	AAU30142

ALIGNMENTS

RESULT 1
AAU08673
ID AAU08673 standard; Protein; 135 AA.
XX
AC AAU08673;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse keratinocyte fatty acid binding protein, Mall.
XX
KW Mouse; Mal 1; keratinocyte fatty acid binding protein; anorectic;
KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
KW dyslipidaemia; atherosclerosis; antisense therapy.
XX
OS Mus musculus.
XX
PN WO200160384-A1.
XX
PD 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US05019.
XX 17-FEB-2000; 2000US-0183106.
XX (HARD) HARVARD COLLEGE.
XX Hotamisligil GS;
XX WPI; 2001-570550/64.
XX N-PSDB; AAS13246.
XX Reducing the level of circulating free fatty acids in a mammal, useful
XX for treating or preventing obesity, diabetes, dyslipidaemia or
XX atherosclerosis, by administering a keratinocyte lipid binding protein
XX inhibitor
XX
XX Disclosure; Page 2; 27pp; English.
XX
XX The invention relates to reducing the level of circulating free fatty
XX acids in a mammal comprising administering to a mammal a compound that
XX inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
XX fatty acid binding protein) or Mall activity. The method is useful for
XX reducing the level of circulating free fatty acids in a mammal,
XX particularly in a mammal that is suffering from or at risk of developing
XX obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
XX useful for diagnosing these diseases. The present sequence is Mouse
XX Mal 1.
XX
XX Sequence 135 AA;
XX
XX Alignment Scores:
XX Pred. No.: 2,36e-37 Length: 135
XX Score: 406.50 Matches: 93
XX Percent Similarity: 45.02% Conservative: 2
XX Best Local Similarity: 44.02% Mismatches: 6
XX Query Match: 18.16% Indels: 110
XX DB: 22 Gaps: 1
XX
XX US-09-788-074-2 (1-1279) x AAU08673 (1-135)
QY 131 GGAGTAGGACTGCTTTAGGAGAGTGGCTGCCATGGCCAGCCAGACTGTATCATTAGC 190
Db 27 GlyValGlyLeuAlaLeuArgLysMetAlaAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACAACATCACGCTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
Db 47 CysAspGlyAsnAsnIleThrValLysThrGluSerThrValLysThrThrValPheSer 66
QY 251 TGTAACTGGGAGAGAAGTTTGATGAACGACAGCTGTATGGCAGAAAAAAGTCAAGTCAAGC 310
Db 67 CysAsnLeuGlyGlyLysPheAspGluThrThrAlaAspGlyArgLysThrGlu-Thr-- 85
QY 311 TACAACATACTGTGAAGCGACAGACAGCTTCTAGATTACAGATTAAATTCATTAACAT 370
Db 85 ----- 85
QY 371 GTCTGTACTTACTGCCAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 85 ----- 85
QY 431 AATTAAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 85 ----- 85
QY 491 GCACATAGTTGTATTGTGNACAAAAATCAGTATCATGGGTGGAGTTTCAGAGAGGAAAGG 550
Db 85 ----- 85
QY 551 CGAAGACTTGTGGAGTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 85 ----- 85

QY 611 TAACTACCTGTATTTTTCAGAGCGGTCTGCACAGCTTCCAGAGGGTGCCTGTGTCACGCA 670
Db 86 -----ValCysThrPheGlnAspGlyAlaLeuValGlnHi 97
QY 671 CCAGCAATGGAGCGGAGAGGAGACGACGATACCAAGAAAACTCAAGGATGGGAAGATGAT 730
Db 97 sGlnGlnTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysMetIi 117
QY 731 CGTGTGTGACATCAAAAGCACTGGCACCATGC 761
Db 117 eValGluCysValMetAsnAlaThrCys 127
RESULT 2
ABG60208
ID ABG60208 standard; Protein; 146 AA.
XX
XX AC ABG60208;
XX
XX DT 30-JUL-2002 (first entry)
XX Human DITHP polypeptide #266.
XX
XX KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
XX cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
XX inflammatory disorder; viral infection; bacterial infection; seizure;
XX fungal infection; parasitic infections; developmental disorder; breast;
XX endocrine disorder; metabolic disorder; neurological disorder; cervix;
XX gastrointestinal disorder; transport disorder; gene therapy; kidney;
XX adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
XX thymus.
XX
XX OS Homo sapiens.
XX
XX PN WO200220754-A2.
XX
XX PD 14-MAR-2002.
XX
XX PF 29-AUG-2001; 2001WO-US27127.
XX
XX PR 05-SEP-2000; 2000US-229747P.
XX PR 05-SEP-2000; 2000US-229748P.
XX PR 05-SEP-2000; 2000US-229749P.
XX PR 05-SEP-2000; 2000US-229750P.
XX PR 05-SEP-2000; 2000US-229751P.
XX PR 05-SEP-2000; 2000US-230583P.
XX PR 05-SEP-2000; 2000US-230505P.
XX PR 05-SEP-2000; 2000US-230514P.
XX PR 05-SEP-2000; 2000US-230515P.
XX PR 05-SEP-2000; 2000US-230517P.
XX PR 05-SEP-2000; 2000US-230518P.
XX PR 05-SEP-2000; 2000US-230519P.
XX PR 05-SEP-2000; 2000US-230595P.
XX PR 05-SEP-2000; 2000US-230597P.
XX PR 05-SEP-2000; 2000US-230598P.
XX PR 05-SEP-2000; 2000US-230599P.
XX PR 05-SEP-2000; 2000US-230610P.
XX PR 05-SEP-2000; 2000US-230865P.
XX PR 05-SEP-2000; 2000US-230988P.
XX PR 05-SEP-2000; 2000US-230951P.
XX PR 05-SEP-2000; 2000US-231163P.
XX PR 05-SEP-2000; 2000US-231167P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
XX Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
XX Momiya MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
XX Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
XX Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI; 2002-383054/41.
XX N-PSDB; ABK71797.
XX

The invention relates to human diagnostic and therapeutic (dithp) polynucleotides and their associated polypeptides (DTHP polypeptides). The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal disorders (e.g. ulcerative colitis, lysinuria) and transport disorders (e.g. myotonic dystrophy, cataractonia, peripheral neuropathy). Sequences ABG59943-ABG60220 represent human DTHP polypeptides of the invention.

AA 16-NOV-1993; 93WO-US11139.
PF

Db 32 GlyValGlyLeuAlaLeuArqLysMetGlyAlaMetAlaLysProAspCysIleIleThr 51

Db 52 LeuAspGlyAsnAsnLeuThrValLysThrGluSerThrValLysThrValPheSer 71

Db 72 CysThrLeuGlyGluLysPheAspGluThrThrAlaAspGlyArqLysThrGlu-Thr-- 90

Db 90 ----- 90

Db 90 ----- 90

Db 90 ----- 90

db 90 ----- 90

Db 90 90

Db 91 -----valCysThrPheThrAspGlyAlaLeuvalGlnHi 102

Db
102 sGlnLysTrpGluGlyLysGluSerThrIleThrArqLysLeuLysAspGlyLysMetVa 122

US-09-788-074-2 (1-1279) x AAR55866 (1-135)

Db 27 GlyValGlyIleAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46

Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66

Db 67 CysThrLeuGlyGluLysPheGluGluThrThrAlaAspGlyArqLysThr-Gln----- 84

84 ----- 84

QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
 Db 84 -----
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTCTTAGATCGAAAA 490
 Db 84 -----
 QY 491 GCACATAGTTGATTGTGAACAAATCAGTATCATGGGTGGAGTTCACAGAGGGAAGG 550
 Db 84 -----
 QY 551 CGAAGACTTGTGGAGTGTGGTCTCGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 84 -----
 QY 611 TAACCTCTGTATTTTGCACAGCGTCTGCACCTTCCAAAGCGTGCCTCGTCCAGCA 670
 Db 85 -----
 QY 671 CCAGCAATGGGAGGAGGACGACGATACAAAGAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGAGCATCAAGCACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127

RESULT 4
 AAU08674
 ID AAU08674 standard; Protein; 135 AA.
 AC AAU08674;
 DT 18-DEC-2001 (first entry)
 DE Human keratinocyte fatty acid binding protein, Mall.
 KW Human; Mall 1; keratinocyte fatty acid binding protein; anorectic;
 KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
 KW dyslipidaemia; atherosclerosis; antisense therapy.
 OS Homo sapiens.
 PN WO200160384-A1.
 PD 23-AUG-2001.
 PF 16-FEB-2001; 2001WO-US05019.
 PR 17-FEB-2000; 2000US-0183106.
 PA (HARD) HARVARD COLLEGE.
 PI Hotamisligil GS;
 DR WPI; 2001-570550/64.
 DR N-PSDB; AAS13247.
 PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidaemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor -
 PS Disclosure; Page 2; 27pp; English.
 CC The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
 CC fatty acid binding protein) or Mall activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also

CC useful for diagnosing these diseases. The present sequence is Human
 CC Mall 1.
 XX
 SQ Sequence 135 AA;
 Alignment Scores:
 Score: 6e-31 Length: 135
 Pred. No.: 350.50 Matches: 78
 Percent Similarity: 41.71% Conservative: 10
 Best Local Similarity: 36.97% Mismatches: 13
 Query Match: 15.65% Indels: 110
 DB: 22 Gaps: 1
 US-09-788-074-2 (1-1279) x AAU08674 (1-135)
 QY 131 GGAGTAGGACTGGCTCTTAGGAGAGATGGTCCATCGCCCAAGCCAGACTGTATCATTCAG 190
 Db 27 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
 QY 191 TGTGATGGCAACAATCATCAGGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCTCT 250
 Db 47 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrGlnPheSer 66
 QY 251 TGTAACTGGGAGAGAGTGTGATGAACGACAGCTGTGTCGCAAGAAACTGAGGTCAGC 310
 Db 67 CysThrLeuGlyGlyLysPheGluGluThrThrAlaAspGlyArgLysThr-Gln----- 84
 QY 311 TACAACATACTGTGAAGCGACAGACAGCTTCTAGATTTACAGATTAATTCATTAACAAT 370
 Db 84 -----
 QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
 Db 84 -----
 QY 431 AATTAGTAAAGTCCAGGACTAAGAAATGAACACATCTTATGAGTTCTTAGATCGAAAA 490
 Db 84 -----
 QY 491 GCACATAGTTGATTGTGAACAAATCAGTATCATGGGTGGAGTTCACAGAGGGAAGG 550
 Db 84 -----
 QY 551 CGAAGACTTGTGGAGTGTGGTCTCGGGTTCCTTCACTTTGGAAGATGATGAAC 610
 Db 84 -----
 QY 611 TAACCTCTGTATTTTGCACAGCGTCTGCACCTTCCAAAGCGTGCCTCGTCCAGCA 670
 Db 85 -----
 QY 671 CCAGCAATGGGAGGAGGACGACGATACAAAGAACTGAAGGATGGGAAGATGAT 730
 Db 97 sGlnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 117
 QY 731 CGTGTGAGCATCAAGCACTGGCACCATGC 761
 Db 117 lValGluCysValMetAsnValThrCys 127
 RESULT 5
 ABG27577
 ID ABG27577 standard; Protein; 158 AA.
 XX
 AC ABG27577;
 XX
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #27568.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS91764.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
XX Claim 20; SEQ ID No 57936; 103pp; English.
XX
XX *The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABC00010-ABC30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from wipo
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 158 AA:
XX
XX Alignment Scores:
XX Pred. No.: 2,398-30 Length: 158
XX Score: 345.50 Matches: 77
XX Percent Similarity: 41.23% Conservative: 10
XX Best Local Similarity: 36.49% Mismatches: 14
XX Query Match: 15.43% Indels: 110
XX DB: 22 Gaps: 1
XX
XX US-09-788-074-2 (1-1279) x ABG27577 (1-158)
XX
XX QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTCAG 190
XX Db 50 GlyValGlyLeuAlaLeuArgLysMetGlyAlaMetProLysPronaspCysIleIleThr 69
XX
XX QY 191 TGTGATGGCAACATCATCGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTCT 250
XX Db 70 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 89
XX
XX QY 251 TGTACCTGGGAGACGAAGTTTCAAGACGACAGCTGATGGCAGAAAACTGAGGTACGC 310
XX Db 90 CysThrLeuGlyGlyLysPheGluGluThrThrAlaAspGlyArgLysThr-Gln----- 107
XX
XX QY 311 TACAACATACTGTGAAGCCAGACAGACCTTCTAGATTACAGATTAAATGTCATTACAT 370
XX Db 107 ----- 107

QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 107 ----- 107
QY 431 AATTAGTAAAGTCCCGAGCTAAGAAATGAACACATCTTATCAGTTTCTAGATCGAAAA 490
Db 107 ----- 107
QY 491 GCACATAGTTGATTGTGAACAAAAATCAGTATGATGGGTGGAGTTTCAGAGAGGGAAGG 550
Db 107 ----- 107
QY 551 CGAAGACTGTTGGAGCTGGTGGTCTGGGTCCTGGGGTTCCTTCACTTTGGAGATGATGAAC 610
Db 107 ----- 107
QY 611 TAACTACCTGTATTTTTCAGACAGCGTCTGCACCTTCCAGAGCGTCCCTGGTCCAGCA 670
Db 108 -----ThrValCysAsnPheThrIleThrArgLysLeuLysAspGlyLysLeuVa 120
QY 671 CCAGCAATGGGAGCGGAGGAGACGACGATACAAAGAACTGAAGGATGGGAAGATGAT 730
Db 120 SGLnGluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVa 140
QY 731 CGTGGTGACATCAAGACGACTGGCACCACATGC 761
Db 140 lValGluCysValMetAsnValThrCys 150
XX
XX RESULT 6
XX ABG61772
XX ID ABG61772 standard; Protein; 135 AA.
XX AC ABG61772;
XX DT 14-AUG-2002 (first entry)
XX DE Novel fatty acid-binding protein-like protein.
XX
XX Cancer; metabolic disorder; skin disorder; infectious disease; anorexia;
XX behavioral disorder; valve disease; endocrine disorder; heart disorder;
XX blood disorder; anxiety disorder; brain disorder; inflammatory disorder;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX immune disorder; haematopoietic disorder; dyslipidaemia;
XX metabolic disturbance; obesity; metabolic syndrome X; wasting disorder;
XX gene therapy; transgenic animal; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200229058-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 05-OCT-2001; 2001WO-US31248.
XX
XX PR 05-OCT-2000; 2000US-238323P.
XX PR 05-OCT-2000; 2000US-238325P.
XX PR 06-OCT-2000; 2000US-238372P.
XX PR 06-OCT-2000; 2000US-238373P.
XX PR 06-OCT-2000; 2000US-238379P.
XX PR 06-OCT-2000; 2000US-238382P.
XX PR 06-OCT-2000; 2000US-238383P.
XX PR 06-OCT-2000; 2000US-238384P.
XX PR 06-OCT-2000; 2000US-238397P.
XX PR 06-OCT-2000; 2000US-238400P.
XX PR 06-OCT-2000; 2000US-238401P.
XX PR 06-OCT-2000; 2000US-238402P.
XX PR 14-MAR-2001; 2001US-275892P.
XX PR 08-JUN-2001; 2001US-296860P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Taupler RJ, Burgess CE, Zerhusen BD, Mezes PS;
XX PI

PI Rastelli L, Malyankar UM, Grosse WM, Alsobrook JP, Lepley DM;
PI Spytek KA, Li L, Edinger S, Gerlach V, Ellerman K, Macdougall J;
PI Gunther E, Millet I, Stone D, Smithson G, Szekeres ES;
XX
DR WPI: 2002-444103/47.
DR N-PSDB; ABK92039.
XX
PT Novel isolated polypeptide, designated NOVX, useful for treating or
PT preventing cancer, diabetes, obesity, dyslipidaemia, anorexia, and
PT metabolic, neurodegenerative, immune and hematopoietic disorders -
XX
PS Claim 1; Page 42; 316pp; English.
XX
CC The invention describes an isolated polypeptide (I), useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease. (I), the polynucleotide encoding it (II) and an antibody
CC (III) to (I) are useful for treating or preventing cancer, metabolic
CC disorders, skin disorders, infectious disease, anorexia, behavioral
CC disorders, valve diseases, endocrine disorders, heart and blood
CC disorders, anxiety disorders, brain disorders, inflammatory disorders,
CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, and the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases. (I), (II) or (III) are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g., diagnostic assays and prognostic assays), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) is
CC useful as immunogen to produce antibodies immunospecific for (I), to
CC screen for potential agonist and antagonist compounds, and as bait
CC protein in a two-hybrid or three-hybrid assay. (II) is useful in gene
CC therapy, to express (I), to detect (I) mRNA or a genetic lesion in a (I)
CC gene, and to modulate activity of (I). A cell containing a vector
CC expressing (I) is useful for producing non-human transgenic animals.
CC This is the amino acid sequence of a novel human polypeptide described
CC in the invention.

XX Sequence 135 AA;

Alignment Scores:

Pred. No.: 2,39e-29 Length: 135
Score: 336.50 Matches: 75
Percent Similarity: 41.23% Conservative: 12
Best Local Similarity: 35.53% Mismatches: 14
Query Match: 15.03% Indels: 110
DB: 23 Gaps: 1

US-09-788-074-2 (1-1279) x ABG61772 (1-135)

QY 131 GGAGTAGGACTGCTTTAGGAAGATGGTCCATGGCCAGCCAGACTGTATCATTCAG 190
DB 27 GLYValGlyIleAlaLeuGlnLysMetGlyAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACAATCAGCTGCTAAACCGAGACAGACAGTGAAGACGACTGTGTTCTCT 250
DB 47 CysAspGlyArgAsnLeuThrLysThrGluSerThrLeuLysThrThrGlnPheSer 66
QY 251 TGTAACTCGGAGAGAGTTTGTATGAACGACAGCTGATGGCAGAAAACACTGAGGTCACC 310
DB 67 CysThrLeuGlyAspGluPheGluGluThrThrAlaAspGlyArgLysThr-Gln----- 84
QY 311 TACAACATACTGTGAAGCGACAGAGACTTCTAGATTACAGATTAAATTCACATTAACAAT 370
DB 84 ----- 84
QY 371 GTCTGTACTACTGCCAAGGGCTGACTGAAAAAATACTTTATGGAGTTGACTTTTGATA 430
DB 84 ----- 84
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAAA 490
DB 84 ----- 84

QY 491 GCACATAGTGTATTGTGTAACAAAATCAGTATGATGGGTGGAGTTCCAGAGAGGAAAGG 550
DB 84 ----- 84
QY 551 CGAAGACTTGTGGAGTGGTGGTCTGGTCTGGGGTTCCTTCACCTTTGGAAGATGATGAAC 610
DB 84 ----- 84
QY 611 TAACTACCCTGTATTTTTCAGACAGCGTCTGACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
DB 85 -----ThrValCysAsnPheThrAspGlyAlaLeuValGlnHl 97
QY 671 CCAGCAATGGGCGGAGGAGGACGACGATACAAAGAAACTGAAGATGGGAGATGAT 730
DB 97 sGlnGluTTPAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuVal 117
QY 731 CGTGGTGACATCAAGCACTGGCACCATGC 761
DB 117 lValGluCysValMetAsnValThrCys 127
RESULT 7
AAU08666
ID AAU08666 standard; Protein; 134 AA.
AC AAU08666;
DT 18-DEC-2001 (first entry)
XX Human NOV10 protein.
XX Human; NOV10; cytostatic; nootropic; neuroprotective; vulnery;
KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
KW antidiabetic; antipsoriatic; antiinflammatory; immunosuppressive;
KW antiatherosclerotic; dermatological; cancer; neurological disorder;
KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW immune disorder; autoimmune disease; respiratory disorder;
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
KW cell growth regulation disorder; lesional psoriatic skin;
KW atherosclerosis; abdominal aortic aneurysm.
XX Homo sapiens.
OS XX
PN WO200168851-A2.
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US07735.
XX
PR 10-MAR-2000; 2000US-0188277.
PR 10-MAR-2000; 2000US-0188316.
PR 14-MAR-2000; 2000US-0189139.
PR 14-MAR-2000; 2000US-0189140.
PR 17-MAR-2000; 2000US-0190231.
PR 17-MAR-2000; 2000US-0190401.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigar M, Vernet CAM, Fernandes E, Shinkets RA, Spaderna SK;
PI Majumder K, Li L;
XX
DR WPI: 2001-570869/64.
DR N-PSDB; AAS13344.
XX
PT Novel polypeptides and nucleic acids homologous to members of collagen,
PT potassium channel, tufelin family of proteins for diagnosing, treating
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders
XX
PS Claim 1; Page 37; 128pp; English.
XX
CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC and anti-NOVX antibodies are useful for treating or preventing a

CC pathology associated with NOVX polypeptide in humans and for treating a
CC syndrome associated with human disease e.g. disorders characterised by
CC altered cell motility, proliferation and migration e.g. cancer,
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC asthma, hypertension and seizure (NOV4), enamel defects, such as
CC amelogenesis imperfecta and disorders involving enamel defects,
CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC encephalitis occurring during testicular cancer, diabetes, reproductive
CC health, metabolic and endocrine disorders, gastrointestinal disorders,
CC immune disorders and autoimmune diseases, respiratory disorders, bone
CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
CC binds to it and a cell expressing NOVX polypeptide is useful for
CC identifying a therapeutic agent for use in treatment of a NOVX related
CC pathology. The antibodies and a polypeptide having 95% sequence identity
CC to NOVX polypeptide are useful for treating a pathological state in a
CC mammal. The present sequence represents NOV10, a possible epidermal
CC fatty acid-binding protein family member.
XX
SQ •Sequence 134 AA;

Alignment Scores:
Pred. No.: 3,12e-25 Length: 134
Score: 300.50 Matches: 68
Percent Similarity: 39.80% Conservative: 12
Best Local Similarity: 33.83% Mismatches: 11
Query Match: 13.42% Indels: 110
DB: 22 Gaps: 1

US-09-788-074-2 (1-1279) x AAU08666 (1-134)

QY 131 GGAGTAGGACTGGCTCTTAGGAGATGGCTGCCATGGCCAGCCAGCTGTATCATTCAG 190
Db 27 G1yValG1yLeuSerLeuArgAsnMetG1yAlaMetAlaLysProAspCysIleIleThr 46
QY 191 TGTGATGGCAACATCATCGGTCAAAACCGAGACAGCAGTGAAGACGACTGTGTTCTCT 250
Db 47 CysAspG1yLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 66
QY 251 TGTAACTCGGAGAGAGTTTGTGATGAACACACAGCTGATGGCAGAAAACTGAGGTCAGC 310
Db 67 CysThrLeuG1yG1yLysPheGluG1yThrThrAlaValG1yArgLysThr-Gln----- 84
QY 311 TACAACACTACTGTGAAGCCGACAGAACTTCTAGATTACAGATTAAATTCGATTAAACAAT 370
Db 84 ----- 84
QY 371 GTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATGAGTTGACTTTTGATA 430
Db 84 ----- 84
QY 431 AATTAGTAAAGTCCAGGACTAAGAAATCAAGACATCTTATGAGTTTCTAGATCGAAAA 490
Db 84 ----- 84
QY 491 GCACATAGTTGATTGTGACAAAATCAGTATGATGGGTGGAGTTCAGAGCGGGAAGG 550
Db 84 ----- 84
QY 551 CGAAGACTGTTGGAGCTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAAC 610
Db 84 ----- 84
QY 611 TAACTACCTGTATTTTGGACAGCGTCTGCACCTTCCAAAGCGGTGCCCTGGTCCAGCA 670
Db 85 -----ThrValCysSerPheThrAspG1yAlaLeuValProH1 97
QY 671 CCAGCAATCGGACGGGAGGAGACGACGATAAACAGAAAACTGAAGGATGGGAAGATGAT 730

db 97 sG1nG1uTrpAspG1yGluAsnThrIleThrArgLysLeuLysAspAlaSerValVa 117
QY 731 C 731
Db 117 I 117
RESULT 8
AAU08665
ID AAU08665 standard; Protein: 163 AA.
XX AAU08665;
AC AAU08665;
XX
DT 18-DEC-2001 (first entry)
DE Human NOV9 protein.
XX
KW Human; NOV9; cytostatic; nootropic; neuroprotective; vulnary;
KW cerebroprotective; antiparkinsonian; hypotensive; antiasthmatic;
KW antiadrenergic; antipsoriatic; antiinflammatory; immunosuppressive;
KW antiatherosclerotic; dermatological; cancer; neurological disorder;
KW Parkinson's disease; diabetes mellitus; asthma; enamel defect;
KW immune disorder; autoimmune disease; respiratory disorder;
KW bone disorder; musculoskeletal disorders; leukaemia; lymphoma;
KW cell growth regulation disorder; lesional psoriatic skin;
KW atherosclerosis; abdominal aortic aneurysm.
XX
OS Homo sapiens.
XX
PN WO200168851-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US07735.
XX
PR 10-MAR-2000; 2000US-0188277.
PR 10-MAR-2000; 2000US-0188316.
PR 14-MAR-2000; 2000US-0189139.
PR 14-MAR-2000; 2000US-0189140.
PR 17-MAR-2000; 2000US-0190231.
PR 17-MAR-2000; 2000US-0190401.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Vernet CAM, Fernandes E, Shimkets RA, Spaderna SK;
PI Majumder K, Li L;
XX
XX WPI: 2001-570869/64.
DR N-PSDB; AAS13343.
XX
PT Novel polypeptides and nucleic acids homologous to members of collagen,
PT potassium channel, tuftelin family of proteins for diagnosing, treating
PT cancer, atherosclerosis, neurological, skin and enamel defect disorders
XX
PS Claim 9; Page 34; 128pp; English.
XX
CC The invention relates to isolated NOVX (NOVX1-11) polypeptides and
CC the polynucleotides that encode them. NOVX polypeptides, polynucleotides
CC and anti-NOVX antibodies are useful for treating or preventing a
CC pathology associated with NOVX polypeptide in humans and for treating a
CC syndrome associated with human disease e.g. disorders characterised by
CC altered cell motility, proliferation and migration e.g. cancer,
CC angiogenesis and wound healing (NOV1-3), neurological disorders, e.g.
CC episodic ataxia, autosomal dominant myokymia, stroke, Parkinson's
CC disease, Alzheimer's disease, non-insulin dependent diabetes mellitus,
CC asthma, hypertension and seizure (NOV4), enamel defects, such as
CC amelogenesis imperfecta and disorders involving enamel defects,
CC including hypoplasia and hypomineralisation (NOV5-7), paraneoplastic
CC neurological disorders, e.g. paraneoplastic limbic of brain-stem
CC encephalitis occurring during testicular cancer, diabetes, reproductive
CC health, metabolic and endocrine disorders, gastrointestinal disorders,
CC immune disorders and autoimmune diseases, respiratory disorders, bone

CC disorders, musculoskeletal disorders, leukaemia/lymphoma and tissue/cell
CC growth regulation disorders (NOV8), lesional psoriatic skin (NOV9-10) and
CC atherosclerosis, abdominal aortic aneurysm and neurological disorders
CC (NOV11). NOVX polypeptide is also useful for identifying an agent that
CC binds to it and a cell expressing NOVX polypeptide is useful for
CC identifying a therapeutic agent for use in treatment of a NOVX related
CC pathology. The antibodies and a polypeptide having 95% sequence identity
CC to NOVX polypeptide are useful for treating a pathological state in a
CC mammal. The present sequence represents NOV9, a possible epidermal
CC fatty acid-binding protein family member.
XX
SQ Sequence 163 AA;

Alignment Scores: 3.4e-25 Length: 163
Pred. No.: 300.50 Matches: 68
Score: 39.80% Conservative: 12
Percent Similarity: 33.83% Mismatches: 11
Best Local Similarity: 13.42% Indels: 110
Query Match: 22 Gaps: 1
DB:

US-09-788-074-2 (1-1279) x AAU08665 (1-163)

QY 131 GGAGTAGGACTGCTCTTAGGAGATGGTCCATCGGCAAGCCAGCTGATCATACG 190
Db 56 GlyValGlyLeuSerLeuArgAsnMetGlyAlaMetAlaLysProAspCysIleIleThr 75
QY 191 TGTGATGGCAACATCATCGGTCFAAACCAGAGACACAGTGAAGACGCTGGTCTCT 250
Db 76 CysAspGlyLysAsnLeuThrIleLysThrGluSerThrLeuLysThrThrGlnPheSer 95
QY 251 TGTAACTGGGAGAGAGTTTGTATGAACACACAGCTGTATGGCAAAAACCTGAGGTCAGC 310
Db 96 CysThrLeuGlyLysPheGluGlyThrThrAlaValGlyArgLysThr-Gln----- 113
QY 311 TACAACATCTGTGAGCCACAGAACCTCTAGATTACAGATTAAATTGCATTACAAT 370
Db 113 ----- 113
QY 371 GTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGATA 430
Db 113 ----- 113
QY 431 AATTAGTAAAGTCCAGGACTAAGAATTAAGACATCTTATGAGTTCTAGATCGAAAA 490
Db 113 ----- 113
QY 491 GCACATAGTTGTATTCTGAACAAATCAGTATGATGGGTGGATTCACAGAGGGAAGG 550
Db 113 ----- 113
QY 551 CGAAGACTTGTGGAGTGGTGGTCCCTGGGGTTTCCTTCACTTTGGAAGATGATGAAC 610
Db 113 ----- 113
QY 611 TAACCTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGCA 670
Db 114 -----ThrValCysSerPheThrAspGlyAlaLeuValProHi 126
QY 671 CCAGCAATGGGCGGGAAGGACAGACAGCATACAAACAACTGAAGGATGGAAGATGAT 730
Db 126 SGlnGluTrpAspGlyLysGluAsnThrIleThrArgLysLeuLysAspAlaSerValVa 146
QY 731 C 731
Db 146 i 146

RESULT 9
ID ABG13616
XX ABG13616 standard; Protein; 79 AA.
AC
XX ABG13616;

DT 18-FEB-2002 (first entry)
XX Novel human diagnostic protein #13607.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS77803.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 43975; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 79 AA;

Alignment Scores:
Pred. No.: 1.4e-16 Length: 79
Score: 224.00 Matches: 43
Percent similarity: 76.12% Conservative: 8
Best Local Similarity: 64.18% Mismatches: 16
Query Match: 10.00% Indels: 0
DB: 22 Gaps: 0

US-09-788-074-2 (1-1279) x ABG13616 (1-79)

QY 615 TACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTCCCTGGTCCAGACCAG 674
Db 8 PheThrLeuPheLeuGlnThrValCysAsnPheThrAspGlyAlaLeuValGlnHisGln 27
QY 675 CAATGGGACGGGAGGAGACGACGATACAAAGAAACTGAAGGATGGAGATGATCGTG 734
Db 28 GluTrpAspGlyLysGluSerThrIleThrArgLysLeuLysAspGlyLysLeuValVal 47

QY	735	GTGAGCATCAACACACTGGCACCATGCTGGGATTGGGCTCGACGCCACAGTTGTCATAAC	794
		::	
Db	48	ValSerValtysLeuLeuCysLeuSerGlnLeuLeuValCysIleHisSerSerHisAsn	67
QY	795	CACTTCGGGTCATTGGTCTTT	815
		:::	
Db	68	CysSerIleSerLeuIleIle	74
RESULT 10			
ABGI3615			
ID	ABGI3615	standard; Protein; 522 AA.	
XX			
AC	ABGI3615;		
XX			
DT	18-FEB-2002	(first entry)	
XX			
DE	Novel human diagnostic protein #13606.		
XX			
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder.		
XX			
OS	Homo sapiens.		
XX			
PN	_WO200175067-A2.		
XX			
PD	11-OCT-2001.		
XX			
PF	30-MAR-2001; 2001WO-US08631.		
XX	†		
PR	31-MAR-2000; 2000US-0540217.		
XX	23-AUG-2000; 2000US-0649167.		
XX			
PA	(HYSE-) HYSBQ INC.		
XX			
PI	Drmanac RT; Liu C; Tang YT;		
XX			
DR	WPI; 2001-639362/73.		
DR	N-PSDB; AAS77802.		
XX			
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX			
PS	Claim 20; SEQ ID NO 43974; 103pp; English.		
XX			
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. ABG00010-ABG30377 represent novel human		
CC	diagnostic amino acid sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences .		
XX			
SQ	Sequence	522 AA;	

Alignment Scores: 1.17e-15 Length: 522

Pred. No.:

Score:	219.00	Matches:	62
Percent Similarity:	42.71%	Conservative:	20
Best Local Similarity:	32.29%	Mismatches:	48
Query Match:	9.78%	Indels:	62
DB:	22	Gaps:	7
US-09-788-074-2 (1-1279) x ABG13615 (1-522)			
Qy	164	ATGCCCAAGCCAGACTGTATCATTCATTGCTGTGATGGCAACAACATCAGGTCAAAACCGAG	223
Db	1	MetaLalysProAspCysIleIleThrCysAspSerLysAsnLeuThrIleLysThrGlu	20
Qy	224	AGCACATGAAGCAGACTGTGTTCTCTTGTAACTCGGAGAGAAAGTTTGTATGAACACGACA	283
Db	21	SerThrLeuLysThrThrGlnPheSerGlyThrLeuGlyGluLysPheGluGluAsnThr	40
Qy	284	GCTGATGGCAGAAAACCTGAGGTCAGCTACAACATACTGTGAAGCGCACAGAAGCTTCTAG	343
Db	41	AlaAspGlyArgArgThrGln	47
Qy	344	ATTTACAGATTAAATTGCATTAAACAATGCTGTACTTACTGCCAAGGGCTGACTGAAAAA	403
Db	48	-----ThrValCysAsnPheThrAspGly-----	55
Qy	404	ACTACTTTATGGAGTTGACTTTTGTGATAAATTAATAAGTCCAGGACTAAGAAATGAAG	463
Db	56	-----ArgSerGluAspThrGluMetAsn	63
Qy	464	ACATCTTATGAGTTTCTA---GATCGAAAGACACATAGTTGTATTGTGAACAAATCAGT	520
Db	64	ValLeuIleSerAlaLeuGlnGluHisSerSerArgAsnProValLysAsnLeuLeuPhe	83
Qy	521	ATGATGGGTGGAGTTCAGAGAGGGGAAGGCGAAGACTTGTGGACTGGTGGGTCCGTG	580
Db	84	ArgLeuGlyPheArgAlaSerLeuGln	92
Qy	581	GGGTTCTTCACTTTGGAAAGATGATGAACATACTACCTCTATTTTTCGACACGGTCTG	640
Db	93	-----ProThrValAlaSer-----ProLeuSerAlaGlyHisGlyGln	105
Qy	641	CACCTTCCAGACGGTCCCTGGTCCAGCACCAAGCAATGGGCGGGAAGGAGACGAT	700
Db	106	HisSerPro---PheSerProGlyAlaAlaProAlaAlaGlyThrGlu	120
Qy	701	AACAAGAAACTGAAGATGGGAAGATGATCGTGGT	736
Db	121	---ProLysGlyGluProLysGluSerGlyArgGly	131
RESULT 11			
ABG13617			
ID	ABG13617 standard; Protein; 181 AA.		
XX	ABG13617;		
AC	AC		
XX	18-FEB-2002 (first entry)		
DT	Novel human diagnostic protein #13608.		
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder.		
XX	Homo sapiens.		
OS	WO200175067-A2.		
XX	11-OCT-2001.		
PN	30-MAR-2001; 2001WO-US08631.		
XX	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
XX	(HYSE-) HYSEQ INC.		
PA	(HYSE-) HYSEQ INC.		

XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS77804.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID No 43976; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 181 AA;

Alignment Scores:

Pred. No.: 4, 13e-13 Length: 181
Score: 195.00 Matches: 64
Percent Similarity: 37.50% Conservative: 14
Best Local Similarity: 30.77% Mismatches: 16
Query Match: 8.71% Indels: 114
DB: 22 Gaps: 7

US-09-788-074-2 (1-1279) x ABG13617 (1-181)

QY 131 GGAGTAGGACTGGCTTGTAGGAAGATGGCTGCCATGGCCAGCCAGAC---TGATATCAT 187
DB 66 GlyValThrIleAlaLeuArgLysMetGlyArgAsnAlaGlnAlaGlnIleCysIleIle 85
QY 188 ACGTGTGTGGCAACAACATCAG---GTCAAACCGAGAGCACAGTGAAGACGACTGTG 244
DB 86 ThrSerAspGly***AsnProSerProLeuTyrThrGluSerThrLeuLysThrThrGln 105
QY 245 TTCTCTTGTAACTG---GGAGAGAAGTTTGATGAACACACAGCTGATGGCAAAACT 301
DB 106 PheSerCysThrLeuTrpGlyGlyLysPheGluGluThrAlaAspGlyGlnLysLys 125
QY 302 GAGGTGAGTACACATACACTGTGAAGCGGACAGAGCTTCTAGATTACAGATTAAATTCG 361
DB 126 -----LeuThrAsnCys 129
QY 362 ATTAACAATGTCTGTACTTACTGCCAAGGGCTGACTGAAAAAATCTATTATGAGCTGA 421
DB 130 -LeuSer----- 131
QY 422 CTTTGTATAAATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTA 481
DB 131 ----- 131
QY 482 GATCGAAAAGCACATAGTTGTATTGTGAACAAATACAGTATGATGGGTGGAGTTCAGAG 541

Db 131 ----- 131
QY 542 AGGGAAGCGAAGACTTGTGGAGTGGTGTGGTCTCTGGGGTTCCTTCACTTTGGAAG 601
Db 131 ----- 131
QY 602 ATGATGAACATACTACCTGCTATTTTTCAGACGGTCTGCACCTTCCAAGACGGTCCCT 661
Db 132 -----ThrPheProAspGlyAlaIle 138
QY 662 GGTCCAGCACCAATGATGGACGGG---AAGGAGACGACGATACAAAGAA---CTGAA 715
Db 138 uValGlnHisGlnGluTrpAspGlyGluArgLysSerThrIleThrLysLysAsn***Ly 158
QY 716 GGATGGGAAGATGATCGTGG 735
Db 158 sAspGlyGluIle-SerTrp 164
RESULT 12
AAW40227
ID AAW40227 standard; Protein; 136 AA.
XX AAW40227;
XX 26-JUN-1998 (first entry)
XX Human myelin P2 protein.
XX Human; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW Guillain-Barre syndrome; vasculitis; nerve inflammation;
KW gammopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 49 /note= "encoded by AAT"
FT
XX
PN WO9803647-A2.
XX 29-JAN-1998.
XX 18-JUL-1997; 97WO-DE01535.
XX 18-JUL-1996; 96DE-1029095.
XX (GOLD/) GOLD R.
PA (WEIS/) WEISHAAPT A.
PI Gold R, Weishaupt A;
DR WPI; 1998-120772/11.
DR N-PSDB; AAV10405.
XX
PT Recombinant myelin proteins for treating T-cell mediated disease of
PT peripheral nervous system - by high dose antigen therapy, causing
PT apoptosis in T cells, for treating e.g. polyneuritis or
PT Guillain-Barre syndrome
XX
PS Disclosure; Fig 4; 14pp; German.
XX
CC The present sequence is the human myelin P2 protein, which can
CC be used to treat T-cell mediated diseases of the peripheral nervous
CC system, especially chronic-inflammatory polyneuritis,
CC Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
CC of gammopathy.
XX
SQ Sequence 136 AA;
Alignment Scores:
Pred. No.: 1.56e-12 Length: 136
Score: 189.50 Matches: 53
Percent Similarity: 34.33% Conservative: 16

Best Local Similarity:	26.37%	Mismatches:	22
Query Match:	8.46%	Indels:	110
DB:	19	Gaps:	1
US-09-788-074-2 (1-1279) x AAU40227 (1-136)			
QY	131	GGAGTAGGACTGGCTCTT	AGGAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTACG 190
DB	25	GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProThrValIleLeuSer 44	
QY	191	TGTGATGGCAACACATCATCGGTCAAAACCGAGACGACAGTGAAGACGACTGTGTCTCT 250	
DB	45	LysLysGlyAspIleleThrIleArgThrGluSerThrPheLysAsnThrGluIleSer 64	
QY	251	TGTAACTCGGAGAGAGTGTGATGAACGACAGCTGATGGCAGAAAACTGAGGTGACG 310	
DB	65	PheLysLeuGlyGlnGluPheGluGluThrThrAlaAspAsnArgLysThr-LysSer-- 83	
QY	311	TACAACATCTGTGAAGCCACAGACCTTCTAGATTACAGATTAATTCGCATTAACAAT 370	
DB	83	-----	-----
QY	371	GTCTGTACTTACTGCCAAGGGCTGACTGAAAAACTTCTTATGGAGTTGACTTTTGATA 430	
DB	83	-----	-----
QY	431	AATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490	
DB	83	-----	-----
QY	491	GCACATAGTTTATTTGTGAACAAATACATGATGGGTGGAGTTCAGAGAGGAAAGG 550	
DB	83	-----	-----
QY	551	CGAAGACTGTTGGAGTGTGTGGTCTCTTCACTTTGGAAGATGATGAAC 610	
DB	83	-----	-----
QY	611	TAACTACCTGTATTTTTCAGACAGCTGTCACCTTCCAAAGCGGTGCTGTCAGCA 670	
DB	84	-----IleValThrLeuGlnArgGlySerLeuAsnGlnVa 95	
QY	671	CGACAAATGGGAGGAGAGACGACGATACACAGAAACTGAAGGATGGGAGATGAT 730	
DB	95	lGlnArgTrpAspGlyLysGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115	
QY	731	C 731	
DB	115	i 115	
RESULT	13		
ID	AAU10059		
XX	AAU10059 standard; Protein; 172 AA.		
AC	AAU10059;		
XX			
DT	14-FEB-2002 (first entry)		
DE	Fatty acid-binding family associated protein, NOV2.		
XX			
KW	NOV; cytosolic; psoriasis; neutropic; neuroprotectant;		
KW	cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;		
KW	haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;		
KW	differentiation; proliferation; haematopoiesis; wound healing;		
KW	angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;		
KW	haemophilia; allergy; Pendred syndrome; skeletal dysplasia;		
KW	ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;		
KW	fatty acid-binding protein; FAPP; chromosome 5.		
OS	Homo sapiens.		
XX			
PN	WO200170978-A2.		
XX			

PD	27-SEP-2001.		
XX			
PF	20-MAR-2001; 2001WO-US09093.		
XX			
PR	20-MAR-2000; 2000US-190768P.		
PR	20-MAR-2000; 2000US-190835P.		
PR	22-MAR-2000; 2000US-190972P.		
PR	22-MAR-2000; 2000US-191199P.		
PR	24-MAR-2000; 2000US-191947P.		
PR	28-MAR-2000; 2000US-192657P.		
PR	28-MAR-2000; 2000US-192664P.		
PR	28-MAR-2000; 2000US-192665P.		
PR	28-MAR-2000; 2000US-192984P.		
PR	29-MAR-2000; 2000US-192836P.		
XX	(CURA-) CURAGEN CORP.		
XX			
PI	Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;		
PI	Vernet CAM;		
XX			
DR	WPI; 2001-639127/73.		
DR	N-PSDB; AAS15722.		
XX			
PT	Polypeptides and nucleic acids related to chloride channel,		
PT	insulin-like growth factor family of proteins, useful for diagnosing		
PT	and treating cancer, cystic fibrosis, acute pancreatitis and		
PT	Alzheimer's disease		
XX			
PS	Claim 1; Page 11; 151pp; English.		
XX			
CC	The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX		
CC	polypeptides are useful for treating pathology associated with NOVX		
CC	polypeptide, determining the presence of or predisposition to a disease		
CC	associated with altered levels of NOVX, identifying agents binding to		
CC	NOVX and treatment of disorders associated with altered expression of		
CC	members of chloride channel-associated proteins e.g. cystic fibrosis and		
CC	congenital myotonia. NOVX proteins are useful in treatment of disorders		
CC	including psoriasis, cancer, diabetes, metabolic disorders of pancreas,		
CC	e.g. acute pancreatitis, abnormal growth and accumulation of mast cells		
CC	in one or more organs (e.g. haemophilia, anaemia), Pendred syndrome,		
CC	skeletal dysplasias, disorders characterised by altered cell shape,		
CC	motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial		
CC	disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the		
CC	treatment of disorders of vascular smooth muscle cell differentiation,		
CC	(e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are		
CC	useful to screen for molecules which inhibit or enhance NOVX activity or		
CC	function and are useful as targets for the identifying small molecules,		
CC	that modulate or inhibit e.g. neurogenesis, proliferation, motility,		
CC	cell differentiation, haematopoiesis, wound healing and angiogenesis. NOV		
CC	sequences are also useful for: identifying a cell or tissue type in a		
CC	biological sample; amplifying DNA sequences from very small biological		
CC	samples e.g. hair or skin or body fluids and as primers and probes to		
CC	identify and/or clone NOVX homologues. NOVX proteins are useful		
CC	immunogens to generate antibodies to monitor protein levels and modulate		
CC	NOVX activity. Cells comprising the nucleic acids are useful for		
CC	producing transgenic animals, for studying the function and/or activity		
CC	of NOVX protein and identifying and/or evaluating modulators of NOVX		
CC	protein activity. This sequence is the NOV2 amino acid sequence (the gene		
CC	is located on chromosome 5) related to the fatty acid-binding protein		
CC	family proteins, one of 12 NOV polypeptides described in the method of		
CC	the invention.		
XX			
SQ	Sequence 172 AA:		
Alignment Scores:			
Pred. No.:	1,24e-11	Length:	172
Score:	182.00	Matches:	55
Percent Similarity:	32.51%	Conservative:	11
Best Local Similarity:	27.09%	Mismatches:	24
Query Match:	8.13%	Indels:	113
DB:	22	Gaps:	3
US-09-788-074-2 (1-1279) x AAU10059 (1-172)			

```
QY 131 GGAGTAGGACTGGCTCTT---AGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTT 187
D 131 |||||
D 65 GlyValGlyLeuAlaLeuCysGluLysGlyAlaMetAlaLysLysAspCysIleSer 84
QY 188 ACGTGTGATGCAACAACATCAGGTCAAAACGAGACGACGTGAAGACGACTGTGCTTC 247
D 188 |||||
D 85 PhePheAspGlyLysAsnLeuThrIleLysMetGluSerThrLeuLysSerTyrSerPhe 104
QY 248 TCTTGTAACTGGGAGAGAAGTTTGTGAACACACACACTGATGCGCAAAAACCTGAGTC 307
D 248 |||
D 105 LeuThrLeuArgGlyGlyLysPheLysGluThrThrGlyAspGlyArgLysThrGln-Th 124
QY 308 AGCTAACACATACTGTGAAGCGACAGAAGCTTCTAGATTTACAGATTAATGCATTAA 367
D 308 ;
D 124 r----- 124
QY 368 AATGCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACITTTG 427
D 368 ----- 124
QY 428 ATAAATAGTAAAGTCCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGA 487
D 428 ----- 124
QY 488 AAGCACATAGTTGATTGTGTGAACAAATCAGTATGATGGGTGGAGTTTCAGAGAGGAA 547
D 488 ----- 124
QY 548 AGGCAAGACTTGTGGAGTGGTGTGGTCTCTGGGGTTCCTTCACCTTGGGAAGATGATG 607
D 548 ----- 124
QY 608 AACTAACCCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTGCCCTGGTCCA 667
D 608 |||||
D 125 -----CysThrPheThrTyrGlyThrLeuValAr 134
QY 668 GCACCAAGCAATGGACGGGAAGGAGACGACGATACAAAGAAACTGAAGATGGGAAGAT 727
D 668 |||||
D 134 gHisGlnLysTrpAsnGlyLysGluGlyLysIle---ArgLysLeuLysAspArgLysLe 153
QY 728 GATCGTG 734
D 728 |||||
D 153 uValVal 155
RESULT 14
AAW40228
ID AAW40228 standard; Protein; 136 AA.
XX
AC AAW40228;
XX
XX 26-JUN-1998 (first entry)
DT
DE Bovine myelin P2 protein.
XX
KW Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW Guillian-Barre syndrome; vasculitis; nerve inflammation;
KW gammopathy.
XX
OS Bos taurus.
XX
PN WO9803647-A2.
XX
XX 29-JAN-1998.
XX
XX 18-JUL-1997; 97WO-DE01535.
XX
XX 18-JUL-1996; 96DE-1029095.
XX
XX (GOLD/) GOLD R.
XX
XX (WEIS/) WEISHAUP A.
XX
XX Cold R, Weishaupt A;
PI
```

```
XX WPI; 1998-120772/11.
XX
XX Recombinant myelin proteins for treating T-cell mediated disease of
PT peripheral nervous system - by high dose antigen therapy, causing
PT apoptosis in T cells, for treating e.g. polyneuritis or
PT Guillian-Barre syndrome
XX
PS Disclosure; Fig 4; 14pp; German.
XX
XX The present sequence is the bovine myelin P2 protein, which can
CC be used to treat T-cell mediated diseases of the peripheral nervous
CC system, especially chronic-inflammatory polyneuritis,
CC Guillian-Barre syndrome, vasculitis and nerve inflammation in cases
CC of gammopathy.
XX
SQ Sequence 136 AA;
Alignment Scores:
Pred. No.: 3.21e-11 Length: 136
Score: 178.00 Matches: 56
Percent Similarity: 33.19% Conservative: 19
Best Local Similarity: 24.78% Mismatches: 32
Query Match: 7.95% Indels: 119
DB: 19 Gaps: 4
US-09-788-074-2 (1-1279) x AAW40228 (1-136)
QY 131 GGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGACTGTATCATTTACG 190
D 131 |||||
D 25 GlyValGlyLeuAlaThrArgLysLeuGlyAsnLeuAlaLysProValIleIleSer 44
QY 191 TGTGATGGCAACAACATCAGGTCAAAACGAGACGACGTGAAGACGACTGTGCTCTCT 250
D 191 |||||
D 45 LysLysGlyAspIleIleThrIleArgThrGluSerProPheLysAsnThrGluIleSer 64
QY 251 TGTAACTCTGGGAGAGAAGTTTGTATGAACACACACAGCTGATGCGCAAAAACCTGAGGTG 310
D 251 |||||
D 65 PheLysLeuGlyGlnGluPheGluThrThrAlaAspAsnArgLysThr-LysSerTh 84
QY 311 TACAACATCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAATTCATTAACAAT 370
D 311 |||
D 84 rValThrLeuAlaArg----- 89
QY 371 GTCTGTACTTACTGCCAAGGSGTGACTGAAAAAACTATTATGGAGTTGCTTTTCATA 430
D 371 ----- 89
QY 431 AATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAAA 490
D 431 ----- 89
QY 491 GCACATAGTTGTATTGTGTGAACAAATCAGTATGATGGGTGGAGTTCAGAGAGGAAAGG 550
D 491 ----- 89
QY 551 CGAAGACTTCTTGGAGCTGGTGGTCTCGGGGGTTCCTTCACCTTTTGAAGATGATGAAC 610
D 551 ----- 89
QY 611 TAACTACCTGTATTTTTCAGACGGTCTGCACCTTCCCAAGACGGTCCCTGGTCCAGCA 670
D 611 |||||
D 90 -----GlySerLeuAsnGlnVa 95
QY 671 CCAGCAATGGGACGGGAAGAGACGACGATACAAAGAAACTGAAGATGGGGAAGATGAT 730
D 671 |||||
D 95 lGlnLysTrpAspGlyAsnGluThrThrIleLysArgLysLeuValAsnGlyLysMetVa 115
QY 731 CGTG---GTGAGCATCAAAAGCACTGGCCACCATCTGGGATTTGGCCCTGAGC-----CA 781
D 731 |||||
D 115 lValGluCysLysMetLys-----AspValValCysThrArgIlefy 129
QY 782 CAGTTGTGCATAACCCAC 797
```

Db	129	rAspValHisHis 134 : :: valAsnGlyaspValIleThrIleLysSerGluSerThrPheLysAsnThrGluIleSer	64
RESULT 15			
AAAY90320	ID	AAAY90320 standard; Protein; 132 AA.	
XX	AC	AAAY90320;	
XX	DT	22-NOV-2000 (first entry)	
XX	DE	Human AFABP protein sequence.	
XX	KW	AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion; lesion formation inhibition; macrophage; adipocyte; atherosclerosis; serum cholesterol; therapy; human.	
XX	OS	Homo sapiens.	
XX	PN	WO200047734-A1.	
XX	PD	17-AUG-2000.	
XX	PF	11-FEB-2000; 2000MO-US03560.	
XX	PR	12-FEB-1999; 99US-0119880.	
XX	PA	(HARD) HARVARD COLLEGE.	
XX	PI	Lee M, Perrella MA, Hotamisligil GS;	
XX	DR	WPI; 2000-506094/45.	
XX	DR	N-PSDB; AAA37717.	
XX	PT	Reducing expression of adipocyte fatty acid binding protein through administration of a compound is used to inhibit formation of an atherosclerotic lesion .	
XX			

This sequence represents the human AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.

AA	Sequence	132 AA;
SQ		

Alignment Scores:

Pred. No.:	7.98e-11	Length:	132
Score:	174.50	Matches:	50
Percent Similarity:	32.6%	Conservative:	16
Best Local Similarity:	24.73%	Mismatches:	26
Query Match:	7.79%	Indels:	110
DB:	21	Gaps:	1

US-09-788-074-2 (1-1279) x AAY90320 (1-132)

Qy	131	GGATAGGACTGGCTCTT	AGGAAGATGGCTGCCATGCCAAGCCACACTGTATCATACG	190
Db	25	GLyvaicGlyPheAlaThrArgLysValAlaGlyMetAlaLysProAsnMetIleIleSer	44	
Qy	191	TGTGTAGGCCAACACATCATCGGTCAAAACCGGAGAGCACAGTGAAGACGACTGTGTTCTCT	250	

Search completed: November 25, 2002, 10:27:57
Job time : 65 secs

THIS PAGE BLANK (USPTO)

85x2